

-1-
SEQUENCE LISTING

<110> Transkaryotic Therapies, Inc.
von Figura, Kurt
Schmidt, Bernhard
Dierks, Thomas
Heartlein, Michael W.
Cosma, Maria P.
Ballabio, Andrea

<120> DIAGNOSIS AND TREATMENT OF MULTIPLE SULFATASE DEFICIENCY AND
OTHER SULFATASE DEFICIENCIES

<130> 0403

<150> US 60/447,747
<151> 2003-02-11

<160> 95

<170> PatentIn version 3.2

<210> 1
<211> 1180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (20)..(1141)
<223> FGE cDNA

<400> 1
acatggcccg cgggacaac atg gct gcg ccc gca cta ggg ctg gtg tgt gga 52
Met Ala Ala Pro Ala Leu Gly Leu Val Cys Gly
1 5 10

cgt tgc cct gag ctg ggt ctc gtc ctc ttg ctg ctg ctg ctc tcg ctg 100
Arg Cys Pro Glu Leu Gly Leu Val Leu Leu Leu Leu Leu Ser Leu
15 20 25

ctg tgt gga gcg gca ggg agc cag gag gcc ggg acc ggt gcg ggc gcg 148
Leu Cys Gly Ala Ala Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala
30 35 40

ggg tcc ctt gcg ggt tct tgc ggc tgc ggc acg ccc cag cgg cct ggc 196
Gly Ser Leu Ala Gly Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly
45 50 55

gcc cat ggc agt tcg gca gcc gct cac cga tac tcg cgg gag gct aac 244
Ala His Gly Ser Ser Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn
60 65 70 75

gct ccg ggc ccc gta ccc gga gag cgg caa ctc gcg cac tca aag atg 292
Ala Pro Gly Pro Val Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met
80 85 90

gtc ccc atc cct gct gga gta ttt aca atg ggc aca gat gat cct cag 340
Val Pro Ile Pro Ala Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln
95 100 105

ata aag cag gat ggg gaa gca cct gcg agg aga gtt act att gat gcc 388
Ile Lys Gln Asp Gly Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala
110 115 120

ttt tac atg gat gcc tat gaa gtc agt aat act gaa ttt gag aag ttt 436
Phe Tyr Met Asp Ala Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe
125 130 135

gtg aac tca act ggc tat ttg aca gag gct gag aag ttt ggc gac tcc 484
Val Asn Ser Thr Gly Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser
140 145 150 155

ttt gtc ttt gaa ggc atg ttg agt gag caa gtg aag acc aat att caa 532
Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr Asn Ile Gln
160 165 170

cag gca gtt gca gct gct ccc tgg tgg tta cct gtg aaa ggc gct aac 580

Gln	Ala	Val	Ala	Ala	Ala	Pro	Trp	Trp	Leu	Pro	Val	Lys	Gly	Ala	Asn		
			175					180					185				
tgg	aga	cac	cca	gaa	ggg	cct	gac	tct	act	att	ctg	cac	agg	ccg	gat	628	
Trp	Arg	His	Pro	Glu	Gly	Pro	Asp	Ser	Thr	Ile	Leu	His	Arg	Pro	Asp		
		190					195					200					
cat	cca	gtt	ctc	cat	gtg	tcc	tgg	aat	gat	gcg	gtt	gcc	tac	tgc	act	676	
His	Pro	Val	Leu	His	Val	Ser	Trp	Asn	Asp	Ala	Val	Ala	Tyr	Cys	Thr		
	205					210					215						
tgg	gca	ggg	aag	cgg	ctg	ccc	acg	gaa	gct	gag	tgg	gaa	tac	agc	tgt	724	
Trp	Ala	Gly	Lys	Arg		Pro	Thr	Glu	Ala	Glu	Trp	Glu	Tyr	Ser	Cys		
220				225						230					235		
cga	gga	ggc	ctg	cat	aat	aga	ctt	ttc	ccc	tgg	ggc	aac	aaa	ctg	cag	772	
Arg	Gly	Gly	Leu	His	Asn	Arg	Leu	Phe	Pro	Trp	Gly	Asn	Lys	Leu	Gln		
				240				245						250			
ccc	aaa	ggc	cag	cat	tat	gcc	aac	att	tgg	cag	ggc	gag	ttt	ccg	gtg	820	
Pro	Lys	Gly	Gln	His	Tyr	Ala	Asn	Ile	Trp	Gln	Gly	Glu	Phe	Pro	Val		
			255					260					265				
acc	aac	act	ggt	gag	gat	ggc	ttc	caa	gga	act	gcg	cct	gtt	gat	gcc	868	
Thr	Asn	Thr	Gly	Glu	Asp	Gly	Phe	Gln	Gly	Thr	Ala	Pro	Val	Asp	Ala		
		270					275					280					
ttc	cct	ccc	aat	ggt	tat	ggc	tta	tac	aac	ata	gtg	ggg	aac	gca	tgg	916	
Phe	Pro	Pro	Asn	Gly	Tyr	Gly	Leu	Tyr	Asn	Ile	Val	Gly	Asn	Ala	Trp		
	285					290					295						
gaa	tgg	act	tca	gac	tgg	tgg	act	gtt	cat	cat	tct	gtt	gaa	gaa	acg	964	
Glu	Trp	Thr	Ser	Asp	Trp	Trp	Thr	Val	His	His	Ser	Val	Glu	Glu	Thr		
300					305					310					315		
ctt	aac	cca	aaa	ggt	ccc	cct	tct	ggg	aaa	gac	cga	gtg	aag	aaa	ggt	1012	
Leu	Asn	Pro	Lys	Gly	Pro	Pro	Ser	Gly	Lys	Asp	Arg	Val	Lys	Lys	Gly		
				320				325						330			
gga	tcc	tac	atg	tgc	cat	agg	tct	tat	tgt	tac	agg	tat	cgc	tgt	gct	1060	
Gly	Ser	Tyr	Met	Cys	His	Arg	Ser	Tyr	Cys	Tyr	Arg	Tyr	Arg	Cys	Ala		
			335					340					345				
gct	cgg	agc	cag	aac	aca	cct	gat	agc	tct	gct	tcg	aat	ctg	gga	ttc	1108	
Ala	Arg	Ser	Gln	Asn	Thr	Pro	Asp	Ser	Ser	Ala	Ser	Asn	Leu	Gly	Phe		
		350					355					360					
cgc	tgt	gca	gcc	gac	cgc	ctg	ccc	acc	atg	gac	tgacaacca	gggtagtctt	1161				
Arg	Cys	Ala	Ala	Asp	Arg	Leu	Pro	Thr	Met	Asp							
		365				370											
ccccagtcca	aggagcagt																1180
<210>	2																
<211>	374																
<212>	PRT																
<213>	Homo sapiens																
<400>	2																
Met	Ala	Ala	Pro	Ala	Leu	Gly	Leu	Val	Cys	Gly	Arg	Cys	Pro	Glu	Leu		
1				5					10					15			
Gly	Leu	Val	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Cys	Gly	Ala	Ala		
		20						25					30				
Gly	Ser	Gln	Glu	Ala	Gly	Thr	Gly	Ala	Gly	Ala	Gly	Ser	Leu	Ala	Gly		
		35					40					45					
Ser	Cys	Gly	Cys	Gly	Thr	Pro	Gln	Arg	Pro	Gly	Ala	His	Gly	Ser	Ser		
	50					55					60						
Ala	Ala	Ala	His	Arg	Tyr	Ser	Arg	Glu	Ala	Asn	Ala	Pro	Gly	Pro	Val		

65		70		75		80
Pro Gly Glu Arg	Gln Leu Ala His	Ser Lys Met Val	Pro Ile Pro Ala			
	85	90	95			
Gly Val Phe Thr	Met Gly Thr Asp	Asp Pro Gln Ile Lys	Gln Asp Gly			
	100	105	110			
Glu Ala Pro Ala	Arg Arg Val Thr	Ile Asp Ala Phe Tyr	Met Asp Ala			
	115	120	125			
Tyr Glu Val Ser	Asn Thr Glu Phe	Glu Lys Phe Val	Asn Ser Thr Gly			
	130	135	140			
Tyr Leu Thr Glu	Ala Glu Lys Phe	Gly Asp Ser Phe	Val Phe Glu Gly			
	145	150	155			160
Met Leu Ser Glu	Gln Val Lys Thr	Asn Ile Gln Gln	Ala Val Ala Ala			
	165	170	175			
Ala Pro Trp Trp	Leu Pro Val Lys	Gly Ala Asn Trp	Arg His Pro Glu			
	180	185	190			
Gly Pro Asp Ser	Thr Ile Leu His	Arg Pro Asp His	Pro Val Leu His			
	195	200	205			
Val Ser Trp Asn	Asp Ala Val Ala	Tyr Cys Thr Trp	Ala Gly Lys Arg			
	210	215	220			
Leu Pro Thr Glu	Ala Glu Trp Glu	Tyr Ser Cys Arg	Gly Gly Leu His			
	225	230	235			240
Asn Arg Leu Phe	Pro Trp Gly Asn	Lys Leu Gln Pro	Lys Gly Gln His			
	245	250	255			
Tyr Ala Asn Ile	Trp Gln Gly Glu	Phe Pro Val Thr	Asn Thr Gly Glu			
	260	265	270			
Asp Gly Phe Gln	Gly Thr Ala Pro	Val Asp Ala Phe	Pro Pro Asn Gly			
	275	280	285			
Tyr Gly Leu Tyr	Asn Ile Val Gly	Asn Ala Trp Glu	Trp Thr Ser Asp			
	290	295	300			
Trp Trp Thr Val	His His Ser Val	Glu Glu Thr Leu	Asn Pro Lys Gly			
	305	310	315			320
Pro Pro Ser Gly	Lys Asp Arg Val	Lys Lys Gly Gly	Ser Tyr Met Cys			
	325	330	335			
His Arg Ser Tyr	Cys Tyr Arg Tyr	Arg Cys Ala Ala	Arg Ser Gln Asn			
	340	345	350			
Thr Pro Asp Ser	Ser Ala Ser Asn	Leu Gly Phe Arg	Cys Ala Ala Asp			
	355	360	365			
Arg Leu Pro Thr	Met Asp					
	370					

<210> 3
<211> 1122
<212> DNA
<213> Homo sapiens

<400> 3
atggctgcgc ccgcactagg gctggtgtgt ggacgttgcc ctgagctggg tctcgtcctc 60
ttgctgctgc tgctctcgct gctgtgtgga gcggcaggga gccaggaggc cgggaccggt 120
gcgggcgcgg ggtcccttgc gggttcttgc ggctgcggca cgcgccagcg gcctggcgcc 180
catggcagtt cggcagccgc tcaccgatac tcgcgggagg ctaacgctcc gggccccgta 240
cccggagagc ggcaactcgc gcactcaaag atggtcccca tccctgctgg agtatattaca 300
atgggacacag atgatcctca gataaagcag gatggggaag cacctgcgag gagagttact 360
attgatgcct ttacatgga tgcctatgaa gtcagtaata ctgaatttga gaagtttgtg 420
aactcaactg gctatttgac agaggctgag aagtttggcg actcctttgt ctttgaaggc 480
atgttgagtg agcaagtga gaccaatatt caacaggcag ttgcagctgc tccctggtgg 540
ttacctgtga aaggcgctaa ctggagacac ccagaagggc ctgactctac tattctgcac 600
aggccggatc atccagttct ccattgtgtc tgggaatgat cggttgccca ctgcacttgg 660
gcagggaagc ggctgcccac ggaagctgag tgggaataca gctgtcgagg aggccctgcat 720
aatagacttt tccctggggg caacaaactg cagcccaaag gccagcatta tgccaacatt 780
tggcagggcg agtttccggt gaccaacact ggtgaggatg gcttccaagg aactgcgcct 840
gttgatgcct tccctcccaa tggttatggc ttatacaaca tagtggggaa cgcatgggaa 900
tggacttcag actggtggac tgttcatcat tctgttgaag aaacgcttaa cccaaaagg 960
cccccttctg ggaaagaccg agtgaagaaa ggtggatcct acatgtgcca taggtcttat 1020
tgttacaggt atcgctgtgc tgctcggagc cagaacacac ctgatagctc tgcttcgaat 1080
ctgggattcc gctgtgcagc cgaccgcctg cccaccatgg ac 1122

<210> 4
<211> 2130
<212> DNA
<213> Homo sapiens

<400> 4
acatggcccc cgggacaaca tggctgcgcc cgcactaggg ctggtgtgtg gacgttgccc 60
tgagctgggt ctcgtcctct tgctgctgct gctctcgctg ctgtgtggag cggcaggag 120
ccaggaggcc gggaccggtg cgggcgcggg gtccttgcg ggttcttgcg gctgcggcac 180
gccccagcgg cctggcgccc atggcagttc ggcagccgct caccgatact cgcgggaggc 240
taacgctccg ggccccgtac ccggagagcg gcaactcgcg cactcaaaga tgggtcccat 300
ccctgctgga gtatttaca tgggcacaga tgatcctcag ataaagcagg atggggaagc 360
acctgcgagg agagttacta ttgatgcctt ttacatggat gcctatgaag tcagtaatac 420
tgaatttgag aagtttgtga actcaactgg ctatttgaca gaggctgaga agtttggcga 480
ctcctttgtc tttgaaggca tgttgagtga gcaagtgaag accaatattc aacaggcagt 540
tgcagctgct ccctggtggt tacctgtgaa aggcgctaac tggagacacc cagaagggcc 600
tgactctact attctgcaca ggccggatca tccagttctc catgtgtcct ggaatgatgc 660
ggttgccctac tgcacttggg cagggaagcg gctgcccacg gaagctgagt gggaatacag 720
ctgtcgagga ggctgcata atagactttt cccctggggc aacaaactgc agcccaaagg 780

ccagcattat gccaacattt ggcagggcga ttttccggtg accaacactg gtgaggatgg 840
 cttccaagga actgcgcctg ttgatgcctt ccctcccaat ggttatggct tataacaacat 900
 agtgggggaac gcatgggaat ggacttcaga ctgggtggact gttcatcatt ctgttgaaga 960
 aacgccttaac ccaaaagggtc ccccttctgg gaaagaccga gtgaagaaag gtggatccta 1020
 catgtgccat aggtcttatt gttacaggta tcgctgtgct gctcggagcc agaacacacc 1080
 tgatagctct gcttcgaatc tgggattccg ctgtgcagcc gaccgcctgc ccaccatgga 1140
 ctgacaacca agggtagtct tccccagtcc aaggagcagt cgtgtctgac ctacattggg 1200
 ctttcctcag aactttgaac gatcccatgc aaagaattcc caccctgagg tgggttacat 1260
 acctgcccac tggccaaagg aaccgccttg tgagaccaa ttgctgacct gggtcagtgc 1320
 atgtgcttta tgggttggtg catctttgga gatcatcacc atattttact tttgagagtc 1380
 tttaaagagg aaggggagtg gagggaaacc tgagctagtc ttcaggaggc ccgcatacta 1440
 cgcaggtctt gccacagggg ttagacccca ggtccgacgc ttgaccttcc tgggcctcaa 1500
 gtgccctccc ctatcaaag aaggaatgga cagcatgacc tctgggtgtc tctccaactc 1560
 accagttcta aaaaggggat cagattctat tgtgacttca tagaatttat gatagattat 1620
 tttttagcta ttttttccat gtgtgaacct tgagtgatac taatcatgta aagtaagagt 1680
 tctcttatgt attatgttcg gaagaggggt gtggtgactc ctttatattc gtactgcact 1740
 ttgtttttcc aaggaaatca gtgtctttta cgttggttatg atgaatccca catggggccg 1800
 gtgatgggat gctgaagttc agccgttgaa cacataggaa tgtctgtggg gtgactctac 1860
 tgtgctttat cttttaacat taagtgcctt tggttcagag gggcagtcac aagctctggt 1920
 tccccctctc cccaaagcct tcagcgaacg tgaaatgtgc gctaaacggg gaaacctggt 1980
 taattctaga tatagggaaa aaggaacgag gaccttgaat gagctatatt cagggtatcc 2040
 ggtattttgt aatagggaat aggaaacctt gttggctgtg gaatatccga tgctttgaat 2100
 catgcactgt gttgaataaa cgtatctgct 2130

<210> 5
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 5

Met Ala Ala Pro Ala Leu Gly Leu Val Cys Gly Arg Cys Pro Glu Leu
 1 5 10 15

Gly Leu Val Leu Leu Leu Leu Leu Ser Leu Leu Cys Gly Ala Ala
 20 25 30

Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala Gly Ser Leu Ala Gly
 35 40 45

Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly Ala His Gly Ser Ser
 50 55 60

Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val
 65 70 75 80

Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala
 85 90 95

Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly
100 105 110

Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala Leu Tyr Met Asp Ala
115 120 125

Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe Val Asn Ser Thr Gly
130 135 140

Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser Phe Val Phe Glu Gly
145 150 155 160

Met Leu Ser Glu Gln Val Lys Thr Asn Ile Gln Gln Ala Val Ala Ala
165 170 175

Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn Trp Arg His Pro Glu
180 185 190

Gly Pro Asp Ser Thr Ile Leu His Arg Pro Asp His Pro Val Leu His
195 200 205

Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr Trp Ala Gly Lys Arg
210 215 220

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys Arg Gly Gly Leu His
225 230 235 240

Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln Pro Lys Gly Gln His
245 250 255

Tyr Ala Asn Ile Trp Gln Gly Asp Phe Pro Val Thr Asn Thr Gly Glu
260 265 270

Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly
275 280 285

Tyr Gly Leu Tyr Asn Ile Val Gly Asn Ala Trp Glu Trp Thr Ser Asp
290 295 300

Trp Trp Thr Val His His Ser Val Glu Glu Thr Leu Asn Pro Lys Gly
305 310 315 320

Pro Pro Ser Gly Lys Asp Arg Val Lys Lys Gly Gly Ser Tyr Met Cys
325 330 335

His Arg Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn
340 345 350

Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly Phe Arg Cys Ala Ala Asp
355 360 365

Arg Leu Pro Thr Met Asp
370

<210> 6
<211> 2297
<212> DNA
<213> Homo sapiens
<400> 6

cggtctgtgtt ggcagctctt catgggttcc cgacgaggag gtctctgtgg ctgcggcggc	60
tgctaactgc gccacctgct gcagcctgtc cccgccgctc tgaagcggcc gcgtcgaagc	120
cgaaatgccg ccaccccgga cgggccgagg ccttctctgg ctgggtctgg ttctgagctc	180
cgtctgcgtc gccctcgat cgaacgca ggccaactcg accacagatg ctctgaacgt	240
tcttctcctc atcgtggatg acctgcgcc ctccttgggc tgttatgggg ataagctggt	300
gaggteccca aatattgacc aactggcctc ccacagcctc ctcttcaga atgcctttgc	360
gcagcaagca gtgtgcgcc cgagccgctt ttctttctc actggcagga gacctgacac	420
caccgcctg tacgacttca actcctactg gagggtgcac gctggaaact tctccaccat	480
ccccagtac ttcaaggaga atggctatgt gacctgtcg gtgggaaaag tctttcacc	540
tgggatattc ttaaccata ccgatgattc tccgtatagc tggctctttc caccttatca	600
tccttctctt gagaagtatg aaaacactaa gacatgtcga gggccagatg gagaactcca	660
tgccaacctg ctttgccctg tggatgtgct ggatgttccc gagggcacct tgcctgacaa	720
acagagcact gagcaagcca tacagttgtt ggaaaagatg aaaacgtcag ccagtccttt	780
cttcttggcc gttgggtatc ataagccaca catcccctc agatacccca aggaatttca	840
gaagtgtgat cccttgaga acatcacctt ggccccgat cccgaggctc ctgatggcct	900
acccctgtg gcctacaacc cctggatgga catcaggcaa cgggaagacg tccaagcctt	960
aaacatcagt gtgccgtatg gtccaattcc tgtggacttt cagcggaaaa tccgccagag	1020
ctactttgcc tctgtgtcat atttggatac acaggctggc cgctcttga gtgctttgga	1080
cgatcttcag ctggccaaca gcaccatcat tgcatttacc tcggatcatg ggtgggctct	1140
aggtgaacat ggagaatggg ccaaatacag caattttgat gttgctacc atgttcccct	1200
gatattctat gttcctggaa ggacggcttc acttcggag gcaggcgaga agcttttccc	1260
ttacctcgac ccttttgatt ccgctcaca gttgatggag ccaggcaggc aatccatgga	1320
ccttgaggaa cttgtgtctc tttttccac gctggctgga cttgcaggac tgcaggttcc	1380
acctcgctgc cccgttcctt catttcacgt tgagctgtgc agagaaggca agaaccttct	1440
gaagcatttt cgattccgtg acttggaaga ggatccgtac ctccctggta atccccgtga	1500
actgattgcc tatagccagt atccccggcc ttcagacatc cctcagtgga attctgacaa	1560
gccgagttta aaagataata agatcatggg ctattccata cgcaccatag actataggta	1620
tactgtgtgg gttggcttca atcctgatga atttctagct aacttttctg acatccatgc	1680
aggggaactg tattttgtgg attctgacct attgcaggat cacaatatgt ataatgattc	1740
ccaagggtga gatcttttcc agttgttgat gccttgagtt ttgccaacca tggatggcaa	1800
atgtgatgtg ctcccttcca gctggtgaga ggaggagtta gagctggctg ttttgtgatt	1860
accataata ttggaagcag cctgagggtt agttaatcca aacatgcac aacaatttgg	1920
cctgagaata tgtaacagcc aaaccttttc gtttagtctt tattaataa tataattggt	1980
aattggacca gttttttttt taatttccct ctttttaaaa cagttacggc ttattttactg	2040
aataaataca aagcaacaa actcaagtta tgtcatacct ttggatacga agaccataca	2100
taataaccaa acataacatt atacacaaag aatactttca ttatttggg aatttagtgc	2160
atttcaaaaa gtaatcatat atcaactag gcaccacact aagttcctga ttattttgtt	2220
tataatttaa taatatatct tatgagccct atatatcaa aatattatgt taacatgtaa	2280
tccatgtttc tttttcc	2297

<210> 7
<211> 550
<212> PRT
<213> Homo sapiens

<400> 7

Met Pro Pro Pro Arg Thr Gly Arg Gly Leu Leu Trp Leu Gly Leu Val
1 5 10 15
Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn Ser
20 25 30
Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg
35 40 45
Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile
50 55 60
Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln
65 70 75 80
Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg
85 90 95
Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His
100 105 110
Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr
115 120 125
Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn
130 135 140
His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro
145 150 155 160
Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly
165 170 175
Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro
180 185 190
Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu
195 200 205
Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly
210 215 220
Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys
225 230 235 240
Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro
245 250 255
Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln
260 265 270
Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile
275 280 285

Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val
290 295 300

Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp
305 310 315 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly
325 330 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp
340 345 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala
355 360 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe
370 375 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu
385 390 395 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu
405 410 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys
420 425 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu
435 440 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser
450 455 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro
465 470 475 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp
485 490 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala
500 505 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp
515 520 525

Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu
530 535 540

Phe Gln Leu Leu Met Pro
545 550

<210> 8

<211> 2657

<212> DNA

<213> Homo sapiens

<400> 8

gaattccggg ccatgagctg ccccggtgcc gcctgctgcg cgctgctgct agtcctgggg

ctctgccggg	cgcgtccccg	gaacgcactg	ctgctcctcg	cggatgacgg	aggctttgag	120
agtggcgcg	acaacaacag	cgccatcgcc	accccgacc	tggacgcctt	ggcccgccgc	180
agcctcctct	ttcgcaatgc	cttcacctcg	gtcagcagct	gctctcccag	ccgcgccagc	240
ctcctcactg	gcctgcccc	gcatcagaat	gggatgtacg	ggctgcacca	ggacgtgcac	300
cacttcaact	ccttcgacaa	gggtgcggagc	ctgccgctgc	tgctcagcca	agctgggtgtg	360
cgcacaggca	tcacgaggaa	gaagcacgtg	gggcccggaga	ccgtgtaccc	gtttgacttt	420
gcgtacacgg	aggagaatgg	ctccgtcctc	caggtggggc	ggaacatcac	tagaattaag	480
ctgctcgtcc	ggaaattcct	gcagactcag	gatgaccggc	ctttcttcct	ctacgtcgcc	540
ttccacgacc	cccaccgctg	tgggcactcc	cagccccagt	acggaacctt	ctgtgagaag	600
tttggcaacg	gagagagcgg	catgggtcgt	atcccagact	ggacccccca	ggcctacgac	660
ccactggacg	tgctgggtgc	ttacttcgtc	cccaacaccc	cggcagcccg	agccgacctg	720
gccgctcagt	acaccaccgt	cggccgcatg	gaccaaggag	ttggactggg	gctccaggag	780
ctgcgtgacg	ccggtgtcct	gaacgacaca	ctgggtgatct	tcacgtccga	caacgggatc	840
cccttcccca	gcggcaggac	caacctgtac	tggccggggc	ctgctgaacc	cttactgggtg	900
tcacccccgg	agcacccaaa	acgctggggc	caagtcagcg	aggcctacgt	gagcctccta	960
gacctcacgc	ccaccatctt	ggattgggtc	tcgatcccgt	accccagcta	cgccatcttt	1020
ggctcgaaga	ccatccacct	cactggccgg	tcctcctgc	cggcgctgga	ggccgagccc	1080
ctctggggcca	ccgtctttgg	cagccagagc	caccacgagg	tcaccatgtc	ctaccccatg	1140
cgtccgtgc	agcaccggca	cttcgcctc	gtgcacaacc	tcaacttcaa	gatgcccttt	1200
cccatcgacc	aggacttcta	cgtctcacc	accttcagg	acctcctgaa	ccgcaccaca	1260
gctggtcagc	ccacgggctg	gtacaaggac	ctccgtcatt	actactaccg	ggcgcgctgg	1320
gagctctacg	accggagccg	ggacccccac	gagaccaga	acctggccac	cgacccgcgc	1380
tttgetcagc	ttctggagat	gcttcgggac	cagctggcca	agtggcagtg	ggagaccac	1440
gacccctggg	tgtgcgcccc	cgacggcgtc	ctggaggaga	agctctctcc	ccagtgccag	1500
cccctccaca	atgagctgtg	accatcccag	gaggcctgtg	cacacatccc	aggcatgtcc	1560
cagacacatc	ccacacgtgt	ccgtgtggcc	ggccagcctg	gggagtagtg	gcaacagccc	1620
ttccgtccac	actcccatcc	aaggagggtt	cttccttcct	gtggggtcac	tcttgccatt	1680
gcctggaggg	ggaccagagc	atgtgaccag	agcatgtgcc	cagcccctcc	accaccaggg	1740
gcactgccgt	catggcaggg	gacacagttg	tccttggtgc	tgaacctatg	cccagcacgg	1800
gaattctaga	catacgtggg	ctgcggacag	ggcagcgccc	ccagcccatg	acaagggagt	1860
cttggtttct	ggcttggttt	ggggacctgc	aaatgggagg	cctgaggccc	tcttcaggct	1920
ttggcagcca	cagatacttc	tgaacccttc	acagagagca	ggcaggggct	tcggtgccgc	1980
gtgggcagta	cgcagggtccc	accgacactc	acctgggagc	acggcgccctg	gctcttacca	2040
gcgtctggcc	tagaggaagc	ctttgagcga	cctttgggca	ggtttctgct	tcttctgttt	2100
tgcccatggg	caagtccctg	ttccccaggc	aggtttcagc	tgattggcag	caggctccct	2160
gagtgatgag	cttgaacctg	tggtgtttct	gggcagaagc	ttatcttttt	tgagagtgtc	2220
cgaagatgaa	ggcatggcga	tgcccgctct	ctggcttggg	ttaattcttc	ggtgacactg	2280
gcattgctgg	gtgggtgatgc	ccgtcctctg	gcttgggtta	attcttcggg	gacactggcg	2340
ttgctgggtg	gcaatgcccc	tcctctgggt	tgggttaatt	cttcggtgac	actggcggtg	2400

ctgggtggcg atgcccgccc tctggcttgg gtttaattctt ggatgacgtc ggcgttgctg 2460
 ggagaatgtg ccgttcctgc cctgcctcca cccacctcg gagcagaagc ccggcctgga 2520
 caccctcgg cctggacacc cctcgaagga gagggcgctt ccttgagtag gtgggctccc 2580
 cttgcccttc cctccctatc actccatact ggggtgggct ggaggaggcc acagggcagc 2640
 tattgtaaaa gctttttt 2657

<210> 9
 <211> 502
 <212> PRT
 <213> Homo sapiens

<400> 9

Met Ser Cys Pro Val Pro Ala Cys Cys Ala Leu Leu Leu Val Leu Gly
 1 5 10 15
 Leu Cys Arg Ala Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp
 20 25 30
 Gly Gly Phe Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro
 35 40 45
 His Leu Asp Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe
 50 55 60
 Thr Ser Val Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly
 65 70 75 80
 Leu Pro Gln His Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His
 85 90 95
 His Phe Asn Ser Phe Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser
 100 105 110
 Gln Ala Gly Val Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro
 115 120 125
 Glu Thr Val Tyr Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser
 130 135 140
 Val Leu Gln Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg
 145 150 155 160
 Lys Phe Leu Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala
 165 170 175
 Phe His Asp Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr
 180 185 190
 Phe Cys Glu Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro
 195 200 205
 Asp Trp Thr Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr
 210 215 220
 Phe Val Pro Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr
 225 230 235 240

Thr Thr Val Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu
245 250 255

Leu Arg Asp Ala Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser
260 265 270

Asp Asn Gly Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro
275 280 285

Gly Thr Ala Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg
290 295 300

Trp Gly Gln Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro
305 310 315 320

Thr Ile Leu Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe
325 330 335

Gly Ser Lys Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu
340 345 350

Glu Ala Glu Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His
355 360 365

Glu Val Thr Met Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe
370 375 380

Arg Leu Val His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln
385 390 395 400

Asp Phe Tyr Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr
405 410 415

Ala Gly Gln Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr
420 425 430

Arg Ala Arg Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr
435 440 445

Gln Asn Leu Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu
450 455 460

Arg Asp Gln Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val
465 470 475 480

Cys Ala Pro Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln
485 490 495

Pro Leu His Asn Glu Leu
500

<210> 10

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 10

cgtgcctgta atcccagcag ctactcactc aggaggctga ggcaggagaa tctcttgaac 60

ccggaaggca gaggttgcag tgagccaaga tcgcgccact gaactccagc ctgggtgaca 120

gagtgaact gtctcagaac agcaacaaca aaatgccgcg tgctgctggg tccagaagag 180
 cttgaataac tgcattgtct ttttctcaat tttcatttcc cagaactggg cacctccggg 240
 ctgtgaaaag ttagggaagt gtctgacacc tccagaatcc attcccaaga agtgcctctg 300
 gtcccactag cacctgcgca gactcaggcc aggcctagaa tctccagttg gccctgcaag 360
 tgcctggagg aaggatggct ctggcctcgg tcttccccca accctgcccc agccagacag 420
 acagcacctg cagacgcagg gggactgcac aattccacct gccaggacc tgaccctggc 480
 gtgtgcttgg cctcctcct cgcccacggc gcctcagatt tcaggaccct cctcctcgcc 540
 caggcgccct cagacctcag gaccctgccg tctcagcct ttgtgaacct caaatatctg 600
 agaccagtct cagtttattt tgccaagggt aaggatgcac ctgtgacagc ctcaggaggt 660
 cctgacaaca ggtgcccag gtggctgggg atacagtttg cctttataca tcttagggag 720
 acacaagatc agtatgtgta tggcgtagat tgggttcagtc agccttccac tgaatacacg 780
 attgagtctg gccagtgaa tccgcatttt tatgtaaaca gtaagggaac ggggcaatca 840
 tataagcgtt tgtctcagg gagccccaga gggatgactt ccagttccgt ctgtcctttg 900
 tccacaagga atttccctgg gcgctaatta tgagggaggc gtgtagcttc ttatcattgt 960
 agctatgtta tttagaaata aaacgggagg caggtttgcc taattcccag gttg 1014

<210> 11
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 11

Met Ala Ala Val Val Ala Ala Thr Arg Trp Trp Gln Leu Leu Leu Val
 1 5 10 15

Leu Ser Ala Ala Gly Met Gly Ala Ser Gly Ala Pro Gln Pro Pro Asn
 20 25 30

Ile Leu Leu Leu Leu Met Asp Asp Met Gly Trp Gly Asp Leu Gly Val
 35 40 45

Tyr Gly Glu Pro Ser Arg Glu Thr Pro Asn Leu Asp Arg Met Ala Ala
 50 55 60

Glu Gly Leu Leu Phe Pro Asn Phe Tyr Ser Ala Asn Pro Leu Cys Ser
 65 70 75 80

Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Ile Arg Asn Gly
 85 90 95

Phe Tyr Thr Thr Asn Ala His Ala Arg Asn Ala Tyr Thr Pro Gln Glu
 100 105 110

Ile Val Gly Gly Ile Pro Asp Ser Glu Gln Leu Leu Pro Glu Leu Leu
 115 120 125

Lys Lys Ala Gly Tyr Val Ser Lys Ile Val Gly Lys Trp His Leu Gly
 130 135 140

His Arg Pro Gln Phe His Pro Leu Lys His Gly Phe Asp Glu Trp Phe
 145 150 155 160

Gly	Ser	Pro	Asn	Cys	His	Phe	Gly	Pro	Tyr	Asp	Asn	Lys	Ala	Arg	Pro	165	170	175
Asn	Ile	Pro	Val	Tyr	Arg	Asp	Trp	Glu	Met	Val	Gly	Arg	Tyr	Tyr	Glu	180	185	190
Glu	Phe	Pro	Ile	Asn	Leu	Lys	Thr	Gly	Glu	Ala	Asn	Leu	Thr	Gln	Ile	195	200	205
Tyr	Leu	Gln	Glu	Ala	Leu	Asp	Phe	Ile	Lys	Arg	Gln	Ala	Arg	His	His	210	215	220
Pro	Phe	Phe	Leu	Tyr	Trp	Ala	Val	Asp	Ala	Thr	His	Ala	Pro	Val	Tyr	225	230	235
Ala	Ser	Lys	Pro	Phe	Leu	Gly	Thr	Ser	Gln	Arg	Gly	Arg	Tyr	Gly	Asp	245	250	255
Ala	Val	Arg	Glu	Ile	Asp	Asp	Ser	Ile	Gly	Lys	Ile	Leu	Glu	Leu	Leu	260	265	270
Gln	Asp	Leu	His	Val	Ala	Asp	Asn	Thr	Phe	Val	Phe	Phe	Thr	Ser	Asp	275	280	285
Asn	Gly	Ala	Ala	Leu	Ile	Ser	Ala	Pro	Glu	Gln	Gly	Gly	Ser	Asn	Gly	290	295	300
Pro	Phe	Leu	Cys	Gly	Lys	Gln	Thr	Thr	Phe	Glu	Gly	Gly	Met	Arg	Glu	305	310	315
Pro	Ala	Leu	Ala	Trp	Trp	Pro	Gly	His	Val	Thr	Ala	Gly	Gln	Val	Ser	325	330	335
His	Gln	Leu	Gly	Ser	Ile	Met	Asp	Leu	Phe	Thr	Thr	Ser	Leu	Ala	Leu	340	345	350
Ala	Gly	Leu	Thr	Pro	Pro	Ser	Asp	Arg	Ala	Ile	Asp	Gly	Leu	Asn	Leu	355	360	365
Leu	Pro	Thr	Leu	Leu	Gln	Gly	Arg	Leu	Met	Asp	Arg	Pro	Ile	Phe	Tyr	370	375	380
Tyr	Arg	Gly	Asp	Thr	Leu	Met	Ala	Ala	Thr	Leu	Gly	Gln	His	Lys	Ala	385	390	395
His	Phe	Trp	Thr	Trp	Thr	Asn	Ser	Trp	Glu	Asn	Phe	Arg	Gln	Gly	Ile	405	410	415
Asp	Phe	Cys	Pro	Gly	Gln	Asn	Val	Ser	Gly	Val	Thr	Thr	His	Asn	Leu	420	425	430
Glu	Asp	His	Thr	Lys	Leu	Pro	Leu	Ile	Phe	His	Leu	Gly	Arg	Asp	Pro	435	440	445
Gly	Glu	Arg	Phe	Pro	Leu	Ser	Phe	Ala	Ser	Ala	Glu	Tyr	Gln	Glu	Ala	450	455	460
Leu	Ser	Arg	Ile	Thr	Ser	Val	Val	Gln	Gln	His	Gln	Glu	Ala	Leu	Val	465	470	475
																		480

Pro Ala Gln Pro Gln Leu Asn Val Cys Asn Trp Ala Val Met Asn Trp
485 490 495

Ala Pro Pro Gly Cys Glu Lys Leu Gly Lys Cys Leu Thr Pro Pro Glu
500 505 510

Ser Ile Pro Lys Lys Cys Leu Trp Ser His
515 520

<210> 12
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 12
ggaattccgg tcggcctctc gcccttcagc tacctgtgcg tccctccgtc ccgtcccgtc 60
ccgggggtcac cccggagcct gtccgctatg cggctcctgc ctctagcccc aggtcggctc 120
cggcggggca gcccccgcca cctgccctcc tgcagcccag cgctgctact gctgggtgctg 180
ggcggtgccc tgggggtctt cgggggtggct gcgggaaccc ggaggcccaa cgtgggtgctg 240
ctcctcacgg acgaccagga cgaagtgtct gcgggcatga caccactaaa gaaaacaaaa 300
gctctcatcg gagagatggg gatgactttt tccagtgtct atgtgccaaag tgetctctgc 360
tgccccagca gagccagtat cctgacagga aagtaccac ataatcatca cgttgtgaac 420
aacactctgg aggggaactg cagtagtaag tcttggcaga agatccaaga accaaatact 480
ttcccagcaa ttctcagatc aatgtgtggt tatcagacct tttttgcagg gaaatattta 540
aatgagtacg gagccccaga tgcaggtgga ctagaacacg ttcctctggg ttggagttac 600
tggtatgcct tggaaaagaa ttctaagtat tataattaca ccctgtctat caatgggaag 660
gcacggaagc atgggtgaaaa ctatagtgtg gactacctga cagatgtttt ggctaattgtc 720
tccttggact ttctggacta caagtccaac tttgagccct tcttcatgat gatcgccact 780
ccagcgctc attcgcttg gacagctgca cctcagtacc agaaggcttt ccagaatgtc 840
tttgcaccaa gaaacaagaa cttcaacatc catggaacga acaagcactg gttaattagg 900
caagccaaga ctccaatgac taattcttca atacagtttt tagataatgc atttaggaaa 960
aggtggcaaa ctctcctctc agttgatgac cttgtggaga aactgggtcaa gaggtggag 1020
ttcactgggg agctcaacaa cacttacatc ttctatacct cagacaatgg ctatcacaca 1080
ggacagtttt ccttgccaat agacaagaga cagctgtatg agtttgatat caaagttcca 1140
ctgttggttc gaggacctgg gatcaaacca aatcagacaa gcaagatgct ggttgccaac 1200
attgacttgg gtccctactat tttggacatt gctggctacg acctaaataa gacacagatg 1260
gatgggatgt ccttattgcc cattttgaga ggtgccagta acttgacctg gcgatcagat 1320
gtcctggtgg aataccaagg agaaggccgt aacgtcactg acccaacatg cccttccttg 1380
agtctggcg tatctcaatg cttcccagac tgtgtatgtg aagatgctta taacaatacc 1440
tatgcctgtg tgaggacaat gtcagcattg tggaatttgc agtattgcga gtttgatgac 1500
caggaggtgt ttgtagaagt ctataatctg actgcagacc cagaccagat cactaacatt 1560
gctaaaacca tagaccacga gcttttagga aagatgaact atcggttaat gatgttacag 1620
tctgtttctg ggccaacctg tcgactcca ggggtttttg accccggata caggtttgac 1680
ccccgtctca tgttcagcaa tcgcggcagt gtcaggactc gaagattttc caaacatctt 1740

ctgtagcgac ctcacacagc ctctgcagat ggatccctgc acgcctcttt ctgatgaagt 1800
gattgtagta ggtgtctgta gctagtcttc aagaccacac ctggaagagt ttctgggctg 1860
gctttaagtc ctgtttgaaa aagcaaccca gtcagctgac ttcctcgtgc aatgtgttaa 1920
actgtgaact ctgcccattgt gtcaggagtg gctgtctctg gtctcttcct ttagctgaca 1980
aggacactcc tgagggtcttt gttctcactg tttttttttt atcctggggc cacagttctt 2040
gattattcct cttgtgggta aagactgaat ttgtaaacc attcagataa atggcagtac 2100
tttaggacac acacaaacac acagatacac cttttgatat gtaagcttga cctaaagtca 2160
aaggacctgt gtagcatttc agattgagca cttcactatc aaaaatacta acatcacatg 2220
gcttgaagag taaccatcag agctgaatca tccaagtaag aacaagtacc attgttgatt 2280
gataagtaga gatacatctt ttatgatgtt catcacagtg tggtaagggt gcaaattcaa 2340
aacatgtcac ccaagctctg ttcattgttt tgtgaattc 2379

<210> 13
<211> 552
<212> PRT
<213> Homo sapiens

<400> 13

Met Arg Leu Leu Pro Leu Ala Pro Gly Arg Leu Arg Arg Gly Ser Pro
1 5 10 15

Arg His Leu Pro Ser Cys Ser Pro Ala Leu Leu Leu Leu Val Leu Gly
20 25 30

Gly Cys Leu Gly Val Phe Gly Val Ala Ala Gly Thr Arg Arg Pro Asn
35 40 45

Val Val Leu Leu Leu Thr Asp Asp Gln Asp Glu Val Leu Gly Gly Met
50 55 60

Thr Pro Leu Lys Lys Thr Lys Ala Leu Ile Gly Glu Met Gly Met Thr
65 70 75 80

Phe Ser Ser Ala Tyr Val Pro Ser Ala Leu Cys Cys Pro Ser Arg Ala
85 90 95

Ser Ile Leu Thr Gly Lys Tyr Pro His Asn His His Val Val Asn Asn
100 105 110

Thr Leu Glu Gly Asn Cys Ser Ser Lys Ser Trp Gln Lys Ile Gln Glu
115 120 125

Pro Asn Thr Phe Pro Ala Ile Leu Arg Ser Met Cys Gly Tyr Gln Thr
130 135 140

Phe Phe Ala Gly Lys Tyr Leu Asn Glu Tyr Gly Ala Pro Asp Ala Gly
145 150 155 160

Gly Leu Glu His Val Pro Leu Gly Trp Ser Tyr Trp Tyr Ala Leu Glu
165 170 175

Lys Asn Ser Lys Tyr Tyr Asn Tyr Thr Leu Ser Ile Asn Gly Lys Ala
180 185 190

Arg Lys His Gly Glu Asn Tyr Ser Val Asp Tyr Leu Thr Asp Val Leu
195 200 205

Ala Asn Val Ser Leu Asp Phe Leu Asp Tyr Lys Ser Asn Phe Glu Pro
210 215 220

Phe Phe Met Met Ile Ala Thr Pro Ala Pro His Ser Pro Trp Thr Ala
225 230 235 240

Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val Phe Ala Pro Arg Asn
245 250 255

Lys Asn Phe Asn Ile His Gly Thr Asn Lys His Trp Leu Ile Arg Gln
260 265 270

Ala Lys Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala
275 280 285

Phe Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu
290 295 300

Lys Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr
305 310 315 320

Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln Phe Ser Leu
325 330 335

Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys Val Pro Leu
340 345 350

Leu Val Arg Gly Pro Gly Ile Lys Pro Asn Gln Thr Ser Lys Met Leu
355 360 365

Val Ala Asn Ile Asp Leu Gly Pro Thr Ile Leu Asp Ile Ala Gly Tyr
370 375 380

Asp Leu Asn Lys Thr Gln Met Asp Gly Met Ser Leu Leu Pro Ile Leu
385 390 395 400

Arg Gly Ala Ser Asn Leu Thr Trp Arg Ser Asp Val Leu Val Glu Tyr
405 410 415

Gln Gly Glu Gly Arg Asn Val Thr Asp Pro Thr Cys Pro Ser Leu Ser
420 425 430

Pro Gly Val Ser Gln Cys Phe Pro Asp Cys Val Cys Glu Asp Ala Tyr
435 440 445

Asn Asn Thr Tyr Ala Cys Val Arg Thr Met Ser Ala Leu Trp Asn Leu
450 455 460

Gln Tyr Cys Glu Phe Asp Asp Gln Glu Val Phe Val Glu Val Tyr Asn
465 470 475 480

Leu Thr Ala Asp Pro Asp Gln Ile Thr Asn Ile Ala Lys Thr Ile Asp
485 490 495

Pro Glu Leu Leu Gly Lys Met Asn Tyr Arg Leu Met Met Leu Gln Ser
500 505 510

Cys Ser Gly Pro Thr Cys Arg Thr Pro Gly Val Phe Asp Pro Gly Tyr
515 520 525

Arg Phe Asp Pro Arg Leu Met Phe Ser Asn Arg Gly Ser Val Arg Thr
530 535 540

Arg Arg Phe Ser Lys His Leu Leu
545 550

<210> 14
<211> 2022
<212> DNA
<213> Homo sapiens

<400> 14
ccggtaccgg ctctcctcgg gctccctcta ggccttccc cccggcccga ctgectggtc 60
agcgccaagt gacttacgcc cccgaccctg agcccggacc gctaggcgag gaggatcaga 120
tctccgctcg agaacttgaa ggtgccctgg tcttgaggga gttccgtccc agccctgcgg 180
tctcccggtg ctgctcgccc cggccctctg gagcttcagg aggcggccgt cagggtcggg 240
gagtatttgg gtccgggggtc tcagggaagg ggcgcgcctg ggtctgcggt atcggaaga 300
gcctgctgga gccaaagtagc cctccctctc ttgggacaga cccctcggtc ccatgtccat 360
gggggcaccg cggtcctctc tcttgccctt ggctgctggc ctggccgttg cccgtccgcc 420
caacatcggtg ctgatctttg ccgacgacct cggctatggg gacctggggt gctatgggca 480
ccccagctct accactccca acctggacca gctggcggcg ggagggctgc ggttcacaga 540
cttctacgtg cctgtgtctc tgtgcacacc ctctagggcc gccctcctga cgggccgggt 600
cccggttcgg atgggcatgt accctggcgt cctgggtgcc agctcccggg ggggcctgcc 660
cctggaggag gtgaccgtgg ccgaagtctt ggctgcccga ggctacctca caggaatggc 720
cggcaagtgg caccttgggg tggggcctga gggggccttc ctgccccccc atcagggtctt 780
ccatcgattt ctaggcattc cgtactccca cgaccagggc ccttgccaga acctgacctg 840
cttcccgccg gccactcctt gcgacggtgg ctgtgaccag ggcttggtcc ccatccact 900
gttgccaac ctgtccgtgg aggcgcagcc cccctggctg cccggactag aggcccgcta 960
catggctttc gccatgacc tcatggccga cggccagcgc caggatcgcc ccttcttctt 1020
gtactatgcc tctcaccaca cccactaccc tcagttcagt gggcagagct ttgcagagcg 1080
ttcaggccgc gggccatttg gggactccct gatggagctg gatgcagctg tggggaccct 1140
gatgacagcc ataggggacc tggggctgct tgaagagacg ctgggtcatct tctactgcaga 1200
caatggacct gagaccatgc gtatgtcccg aggcggctgc tccggtctct tgcgggtgtg 1260
aaaggggaacg acctacgagg gcggtgtccg agagcctgcc ttggccttct ggccagggtca 1320
tatcgctccc ggcgtgacct acgagctggc cagctccctg gacctgctgc ctacctggc 1380
agccctggct ggggccccac tgcccaatgt caccttggat ggctttgacc tcagccccct 1440
gctgctgggc acaggcaaga gccctcggca gtctctcttc ttctaccgt cctaccaga 1500
cgaggctcgt ggggtttttg ctgtgcggac tggaaagtac aaggctcact tcttcacca 1560
gggctctgcc cacagtgata cactgcaga ccctgcctgc cagcctcca gctctctgac 1620
tgctcatgag ccccgctgc tctatgacct gtccaaggac cctggtgaga actacaacct 1680
gctgggggggt gtggccgggg ccacccaga ggtgctgcaa gccctgaaac agcttcagct 1740

gctcaaggcc cagttagacg cagctgtgac cttcggcccc agccaggtgg cccggggcgga 1800
 ggaccccgcc ctgcagatct gctgtcatcc tggctgcacc ccccgcccag cttgctgcca 1860
 ttgcccagat ccccatgcct gagggcccct cggctggcct gggcatgtga tggctcctca 1920
 ctggggagcct gtgggggagg ctcaggtgtc tggaggggggt ttgtgcctga taacgtaata 1980
 acaccagtgg agacttgacac atctgaaaaa aaaaaaaaaa aa 2022

<210> 15
 <211> 507
 <212> PRT
 <213> Homo sapiens

<400> 15

Met Gly Ala Pro Arg Ser Leu Leu Leu Ala Leu Ala Ala Gly Leu Ala
 1 5 10 15

Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly
 20 25 30

Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn
 35 40 45

Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val
 50 55 60

Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg
 65 70 75 80

Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser
 85 90 95

Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala
 100 105 110

Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val
 115 120 125

Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe
 130 135 140

Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr
 145 150 155 160

Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu
 165 170 175

Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro
 180 185 190

Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu
 195 200 205

Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala
 210 215 220

Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu
 225 230 235 240

Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala
245 250 255

Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu
260 265 270

Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg
275 280 285

Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr
290 295 300

Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly
305 310 315 320

His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu
325 330 335

Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr
340 345 350

Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser
355 360 365

Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg
370 375 380

Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr
385 390 395 400

Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala
405 410 415

Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser
420 425 430

Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala
435 440 445

Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala
450 455 460

Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly
465 470 475 480

Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg
485 490 495

Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
500 505

<210> 16
<211> 2228
<212> DNA
<213> Homo sapiens

<400> 16
acaaggatgg gtccgcgcgg cgcggcgagc ttgccccgag gccccggacc tcggcggtg 60
ctcctccccg tcgtcctccc gctgctgctg ctgctgttgt tggcgccgcc gggtcgggc 120

gccggggcca gccggccgcc ccacctggtc ttcttgctgg cagacgacct aggctggaac	180
gacgtcggt tccacggctc ccgcacccgc acgccgcacc tggacgcgct ggccggccggc	240
ggggtgctcc tggacaacta ctacacgcag ccgctgtgca cgccgtcgcg gagccagctg	300
ctcactggcc gctaccagat ccgtacaggt ttacagcacc aaataatctg gccctgtcag	360
cccagctgtg ttctcttgga tgaaaaactc ctgccccagc tcctaaaaga agcaggttat	420
actaccata tggtcggaaa atggcacctg ggaatgtacc ggaaagaatg ccttccaacc	480
cgccgaggat ttgataccta ctttgatat ctctgggta gtgaagatta ttattcccat	540
gaacgctgta cattaattga cgctctgaat gtcacacgat gtgctcttga ttttcgagat	600
ggcgaagaag ttgcaacagg atataaaaat atgtattcaa caacatatt caccaaaagg	660
gctatagccc tcataactaa ccattccacca gagaagcctc tgtttctcta ccttgctctc	720
cagtctgtgc atgagccctc tcaggtccct gaggaatact tgaagccata tgactttatc	780
caagacaaga acaggcatca ctatgcagga atgggtgtccc ttatggatga agcagtagga	840
aatgtcactg cagctttaaa aagcagtggg ctctggaaca acacggtgtt catcttttct	900
acagataacg gagggcagac tttggcaggg ggtaataact ggccccctcg aggaagaaaa	960
tggagcctgt ggaaggagg cgcccgagg gtgggctttg tggcaagccc cttgctgaag	1020
cagaagggcg tgaagaaccg ggagctcatc cacatctctg actggctgcc aacactcgtg	1080
aagctggcca ggggacacac caatggcaca aagcctctgg atggcttcga cgtgtggaaa	1140
accatcagtg aagggaagccc atccccaga attgagctgc tgcataatat tgacccaaac	1200
ttcgtggact cttcacctg tcccaggaac agcatggctc cagcaaagga tgactcttct	1260
cttcagaat attcagcctt taacacatct gtccatgctg caattagaca tggaaattgg	1320
aaactcctca cgggctaccc aggctgtggg tactgggtcc ctccaccgtc tcaatacaat	1380
gtttctgaga taccctcatc agaccacca accaagacc tctggctctt tgatattgat	1440
cgggaccctg aagaaagaca tgacctgtcc agagaatatc ctcacatcgt cacaaagctc	1500
ctgtcccgcc tacagttcta ccataaacac tcagtcctcg tgtacttccc tgcaacaggac	1560
ccccgctgtg atcccaaggc cactgggggtg tggggccctt ggatgtagga tttcagggag	1620
gctagaaaac ctttcaattg gaagttggac ctcaggcctt ttctcacgac tcttgtctca	1680
tttgttatcc caacctgggt tcaactggcc cttctcttgc tcttaaacca caccgaggtg	1740
tctaatttca acccctaatt catttaagaa gctgataaaa tctgcaacac tcctgctgtt	1800
ggctggagca tgtgtctaga ggtgggggtg gctgggttta tcccccttc ctaagccttg	1860
ggacagctgg gaacttaact tgaaatagga agttctcact gaatcctgga ggctggaaca	1920
gctggctctt ttagactcac aagtcagacg ttcgattccc ctctgccaat agccagtttt	1980
attggagtga atcacatttc ttacgcaa atgaaggagca gacagtgatt aatggttctg	2040
ttggccaagg cttctccctg tcggtgaagg atcatgttca ggcaactcaa gtgaaccacc	2100
cctcttgggt cacccttac tcaattatct catcacagag cataaggccc attttgttgt	2160
tcagggtcaac agcaaaatgg cctgcaccat gactgtggct tttaaaataa agaaatgtgt	2220
ttttatcg	2228

<210> 17
 <211> 533
 <212> PRT
 <213> Homo sapiens

<400> 17

Met	Gly	Pro	Arg	Gly	Ala	Ala	Ser	Leu	Pro	Arg	Gly	Pro	Gly	Pro	Arg	
1				5					10					15		
Arg	Leu	Leu	Leu	Pro	Val	Val	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
			20					25					30			
Ala	Pro	Pro	Gly	Ser	Gly	Ala	Gly	Ala	Ser	Arg	Pro	Pro	His	Leu	Val	
		35					40					45				
Phe	Leu	Leu	Ala	Asp	Asp	Leu	Gly	Trp	Asn	Asp	Val	Gly	Phe	His	Gly	
	50					55					60					
Ser	Arg	Ile	Arg	Thr	Pro	His	Leu	Asp	Ala	Leu	Ala	Ala	Gly	Gly	Val	
65					70					75					80	
Leu	Leu	Asp	Asn	Tyr	Tyr	Thr	Gln	Pro	Leu	Cys	Thr	Pro	Ser	Arg	Ser	
				85					90					95		
Gln	Leu	Leu	Thr	Gly	Arg	Tyr	Gln	Ile	Arg	Thr	Gly	Leu	Gln	His	Gln	
			100					105					110			
Ile	Ile	Trp	Pro	Cys	Gln	Pro	Ser	Cys	Val	Pro	Leu	Asp	Glu	Lys	Leu	
		115					120					125				
Leu	Pro	Gln	Leu	Leu	Lys	Glu	Ala	Gly	Tyr	Thr	Thr	His	Met	Val	Gly	
		130				135					140					
Lys	Trp	His	Leu	Gly	Met	Tyr	Arg	Lys	Glu	Cys	Leu	Pro	Thr	Arg	Arg	
145					150					155					160	
Gly	Phe	Asp	Thr	Tyr	Phe	Gly	Tyr	Leu	Leu	Gly	Ser	Glu	Asp	Tyr	Tyr	
				165					170					175		
Ser	His	Glu	Arg	Cys	Thr	Leu	Ile	Asp	Ala	Leu	Asn	Val	Thr	Arg	Cys	
			180					185						190		
Ala	Leu	Asp	Phe	Arg	Asp	Gly	Glu	Glu	Val	Ala	Thr	Gly	Tyr	Lys	Asn	
		195					200					205				
Met	Tyr	Ser	Thr	Asn	Ile	Phe	Thr	Lys	Arg	Ala	Ile	Ala	Leu	Ile	Thr	
	210					215					220					
Asn	His	Pro	Pro	Glu	Lys	Pro	Leu	Phe	Leu	Tyr	Leu	Ala	Leu	Gln	Ser	
225					230					235					240	
Val	His	Glu	Pro	Leu	Gln	Val	Pro	Glu	Glu	Tyr	Leu	Lys	Pro	Tyr	Asp	
				245					250					255		
Phe	Ile	Gln	Asp	Lys	Asn	Arg	His	His	Tyr	Ala	Gly	Met	Val	Ser	Leu	
			260					265					270			
Met	Asp	Glu	Ala	Val	Gly	Asn	Val	Thr	Ala	Ala	Leu	Lys	Ser	Ser	Gly	
		275					280					285				
Leu	Trp	Asn	Asn	Thr	Val	Phe	Ile	Phe	Ser	Thr	Asp	Asn	Gly	Gly	Gln	
	290					295					300					

Thr Leu Ala Gly Gly Asn Asn Trp Pro Leu Arg Gly Arg Lys Trp Ser
305 310 315 320

Leu Trp Glu Gly Gly Val Arg Gly Val Gly Phe Val Ala Ser Pro Leu
325 330 335

Leu Lys Gln Lys Gly Val Lys Asn Arg Glu Leu Ile His Ile Ser Asp
340 345 350

Trp Leu Pro Thr Leu Val Lys Leu Ala Arg Gly His Thr Asn Gly Thr
355 360 365

Lys Pro Leu Asp Gly Phe Asp Val Trp Lys Thr Ile Ser Glu Gly Ser
370 375 380

Pro Ser Pro Arg Ile Glu Leu Leu His Asn Ile Asp Pro Asn Phe Val
385 390 395 400

Asp Ser Ser Pro Cys Pro Arg Asn Ser Met Ala Pro Ala Lys Asp Asp
405 410 415

Ser Ser Leu Pro Glu Tyr Ser Ala Phe Asn Thr Ser Val His Ala Ala
420 425 430

Ile Arg His Gly Asn Trp Lys Leu Leu Thr Gly Tyr Pro Gly Cys Gly
435 440 445

Tyr Trp Phe Pro Pro Pro Ser Gln Tyr Asn Val Ser Glu Ile Pro Ser
450 455 460

Ser Asp Pro Pro Thr Lys Thr Leu Trp Leu Phe Asp Ile Asp Arg Asp
465 470 475 480

Pro Glu Glu Arg His Asp Leu Ser Arg Glu Tyr Pro His Ile Val Thr
485 490 495

Lys Leu Leu Ser Arg Leu Gln Phe Tyr His Lys His Ser Val Pro Val
500 505 510

Tyr Phe Pro Ala Gln Asp Pro Arg Cys Asp Pro Lys Ala Thr Gly Val
515 520 525

Trp Gly Pro Trp Met
530

<210> 18
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 18
gcttcacgca gctgacggga cccagctgta gtgaggttgc agtgattgag taggattggc 60
ctgcttcaaa gcagaggttt ctcatgggaa tatgcttatt aaactccac tgggtgcagaa 120
accatgaaca gaggatgaac aagtgaagtt gcaatctcct ccatcacagc tcagttcccc 180
aacaacagga tcacaagctg gagatgcctt taaggaagat gaagatccct ttcctcctac 240
tgtttcttct gtgggaagcc gagagccacg cagcatcaag gccgaacatc atcctgggtga 300
tggtgacga cctcggcatt ggagatcctg ggtgctatgg gaacaaaact atcaggactc 360

ccaatatcga ccggttggcc agtgggggag tgaaactcac tcagcacctg gcagcatcac 420
cgctgtgcac accaagcagg gcagccttca tgactggccg gtaccctgtc cgatcaggaa 480
tgccatcttg gtcccgcaact ggagttttcc tcttcacagc ctcttcggga ggacttccca 540
ccgatgagat taccttttgt aagcttctga aggatcaagg ttattcaaca gcaactgatat 600
ggaaatggca ccttgggatg agctgtcaca gcaagactga cttctgtcac caccctttac 660
atcacggcct caattatttc tatgggatct ctttgaccaa tctgagagac tgcaagcccg 720
gagagggcag tgtcttcacc acgggcttca agaggctggg ctctctcccc ctgcagatcg 780
tcggggctac cctccttacc cttgctgcac tcaattgtct ggggctactc cacgtgcctc 840
taggcgtttt tttcagcctt ctcttcctag cagccctaact cctgaccctt ttcttgggct 900
tccttcatta cttccggccc ctgaactgct tcatgatgag gaactacgag atcattcagc 960
agcccatgtc ctatgacaat ctcaccaga ggctaacggg ggaggcggcc cagttcatac 1020
agcggaacac tgagactccg ttctgtcttg tcttgctcta cctccacgtg cacacagccc 1080
tgttctccag caaagacttt gctggcaaaa gtcaacacgg agtctacggg gatgctgttg 1140
aggaaatgga ctggagtgtg gggcagatct tgaaccttct ggatgagctg agattggcta 1200
atgataccct catctacttc acatcggacc agggagcaca tgtagaggag gtgtcttcca 1260
aaggagaaat tcatggcgga agtaatggga tctataaagg aggaaaagca aacaactggg 1320
aaggaggat ccgggttcca ggcaccttc gttggcccag ggtgatacag gctggccaga 1380
agattgatga gccactagc aacatggaca tatttcctac agtagccaag ctggctggag 1440
ctcccttgcc tgaggacagg atcattgatg gacgtgatct gatgccctg cttgaaggaa 1500
aaagccaacg ctccgatcat gagtttctct tccattactg caacgcctac ttaaagtctg 1560
tgcgctggca cctcagaac agcacatcca tctggaaggc ctttttcttc accccaact 1620
tcaaccccg gggttccaac ggatgctttg ccacacacgt gtgcttctgt ttcgggagtt 1680
atgtcaccca tcacgacca cctttactct ttgatatttc caaagatccc agagagagaa 1740
accactaac tccagcatcc gagccccggg tttatgaaat cctcaaagtc atgcaggaag 1800
ctgcggacag acacaccag accctgccag aggtgcccga tcagttttca tggacaact 1860
ttctttggaa gccctggctt cagctgtgct gtccttcac cggcctgtct tgccagtgtg 1920
atagagaaaa acaggataag agactgagcc gctagcagcg cctggggacc agacagacgc 1980
atgtggcaaa gctcaccatc ttcactacaa acacgcctga gagtggcact ggggaaacat 2040
aactccatct acaccttggg tttggactga ttctccattt taccactga aggcttgggc 2100
cagagctcaa cagctactca actggagggg tgagggggat aaggctctgt gtatacagac 2160
aggaagatgg taggtttatg cttctgtgg ccagagtctt ggactcatgg aaatagaatg 2220
aatagagggg cattcacaag gcacaccagt gcaagcagat gacaaaaagg tgcagaaggc 2280
aatcttaaaa cagaaagggt caggaggtac cttaactcac ccctcagcaa atacctatgt 2340
caacagtata agttaccatt tactctataa tctgcagtga tgcaataacc agcataataa 2400
a 2401

<210> 19
<211> 583
<212> PRT
<213> Homo sapiens

<400> 19

Met Pro Leu Arg Lys Met Lys Ile Pro Phe Leu Leu Leu Phe Phe Leu
1 5 10 15

Trp Glu Ala Glu Ser His Ala Ala Ser Arg Pro Asn Ile Ile Leu Val
20 25 30

Met Ala Asp Asp Leu Gly Ile Gly Asp Pro Gly Cys Tyr Gly Asn Lys
35 40 45

Thr Ile Arg Thr Pro Asn Ile Asp Arg Leu Ala Ser Gly Gly Val Lys
50 55 60

Leu Thr Gln His Leu Ala Ala Ser Pro Leu Cys Thr Pro Ser Arg Ala
65 70 75 80

Ala Phe Met Thr Gly Arg Tyr Pro Val Arg Ser Gly Met Ala Ser Trp
85 90 95

Ser Arg Thr Gly Val Phe Leu Phe Thr Ala Ser Ser Gly Gly Leu Pro
100 105 110

Thr Asp Glu Ile Thr Phe Ala Lys Leu Leu Lys Asp Gln Gly Tyr Ser
115 120 125

Thr Ala Leu Ile Gly Lys Trp His Leu Gly Met Ser Cys His Ser Lys
130 135 140

Thr Asp Phe Cys His His Pro Leu His His Gly Phe Asn Tyr Phe Tyr
145 150 155 160

Gly Ile Ser Leu Thr Asn Leu Arg Asp Cys Lys Pro Gly Glu Gly Ser
165 170 175

Val Phe Thr Thr Gly Phe Lys Arg Leu Val Phe Leu Pro Leu Gln Ile
180 185 190

Val Gly Val Thr Leu Leu Thr Leu Ala Ala Leu Asn Cys Leu Gly Leu
195 200 205

Leu His Val Pro Leu Gly Val Phe Phe Ser Leu Leu Phe Leu Ala Ala
210 215 220

Leu Ile Leu Thr Leu Phe Leu Gly Phe Leu His Tyr Phe Arg Pro Leu
225 230 235 240

Asn Cys Phe Met Met Arg Asn Tyr Glu Ile Ile Gln Gln Pro Met Ser
245 250 255

Tyr Asp Asn Leu Thr Gln Arg Leu Thr Val Glu Ala Ala Gln Phe Ile
260 265 270

Gln Arg Asn Thr Glu Thr Pro Phe Leu Leu Val Leu Ser Tyr Leu His
275 280 285

Val His Thr Ala Leu Phe Ser Ser Lys Asp Phe Ala Gly Lys Ser Gln
290 295 300

His Gly Val Tyr Gly Asp Ala Val Glu Glu Met Asp Trp Ser Val Gly
305 310 315 320

Gln Ile Leu Asn Leu Leu Asp Glu Leu Arg Leu Ala Asn Asp Thr Leu
325 330 335

Ile Tyr Phe Thr Ser Asp Gln Gly Ala His Val Glu Glu Val Ser Ser
340 345 350

Lys Gly Glu Ile His Gly Gly Ser Asn Gly Ile Tyr Lys Gly Gly Lys
355 360 365

Ala Asn Asn Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Leu Arg Trp
370 375 380

Pro Arg Val Ile Gln Ala Gly Gln Lys Ile Asp Glu Pro Thr Ser Asn
385 390 395 400

Met Asp Ile Phe Pro Thr Val Ala Lys Leu Ala Gly Ala Pro Leu Pro
405 410 415

Glu Asp Arg Ile Ile Asp Gly Arg Asp Leu Met Pro Leu Leu Glu Gly
420 425 430

Lys Ser Gln Arg Ser Asp His Glu Phe Leu Phe His Tyr Cys Asn Ala
435 440 445

Tyr Leu Asn Ala Val Arg Trp His Pro Gln Asn Ser Thr Ser Ile Trp
450 455 460

Lys Ala Phe Phe Phe Thr Pro Asn Phe Asn Pro Val Gly Ser Asn Gly
465 470 475 480

Cys Phe Ala Thr His Val Cys Phe Cys Phe Gly Ser Tyr Val Thr His
485 490 495

His Asp Pro Pro Leu Leu Phe Asp Ile Ser Lys Asp Pro Arg Glu Arg
500 505 510

Asn Pro Leu Thr Pro Ala Ser Glu Pro Arg Phe Tyr Glu Ile Leu Lys
515 520 525

Val Met Gln Glu Ala Ala Asp Arg His Thr Gln Thr Leu Pro Glu Val
530 535 540

Pro Asp Gln Phe Ser Trp Asn Asn Phe Leu Trp Lys Pro Trp Leu Gln
545 550 555 560

Leu Cys Cys Pro Ser Thr Gly Leu Ser Cys Gln Cys Asp Arg Glu Lys
565 570 575

Gln Asp Lys Arg Leu Ser Arg
580

<210> 20
<211> 1945
<212> DNA
<213> Homo sapiens

<400> 20
ggaagccttg gcactagcgg cgcccgggcg cggagtgcgc agggcaaggt cctgcgctct

gggccagcgc tcggccatgc gatccgccgc gcggagggga cgcgccgcgc ccgccgccag 120
 ggactctttg ccggtgctac tgtttttatg cttgcttctg aagacgtgtg aacctaaaac 180
 tgcaaatgcc tttaaaccaa atatcctact gatcatggcg gatgatctag gcaactgggga 240
 tctcggttgc tacgggaaca atacactgag aacgccgaat attgaccagc ttgcagagga 300
 aggtgtgagg ctcaactcagc acctggcggc cgcgccgctc tgcaccccaa gccgagctgc 360
 attcctcaca gggagacatt ccttcagatc aggcattggac gccagcaatg gataccgggc 420
 ccttcagtgg aacgcaggct cagggtggact ccctgagaac gaaaccactt ttgcaagaat 480
 cttgcagcag catggctatg caaccggcct catagggaaa tggcaccagg gtgtgaattg 540
 tgcattccgc ggggatcact gccaccaccc cctgaaccac ggatttgact atttctacgg 600
 catgcccttc acgctcacia acgactgtga cccaggcagg ccccccgaag tggacgccgc 660
 cctgagggcg cagctctggg gttacaccca gttcctggcg ctggggattc tcacctggc 720
 tgccggccag acctgcggtt tcttctctgt ctccgcgaga gcagtcaccg gcatggccgg 780
 cgtgggctgc ctgtttttca tctcttggtg ctctctcttc gggtttgtgc gacgctggaa 840
 ctgtatcctg atgagaaacc atgacgtcac ggagcaacc atgggttctg agaaaacagc 900
 gagtcttatg ctaaaaggaag ctgtttccta tattgaaaga cacaagcatg ggccatttct 960
 cctcttcctt tctttgctgc atgtgcacat tccccttggt accacgagtg cattcctggg 1020
 gaaaagtcag catggcttat atggtgataa tgtggaggag atggactggc tcataggtaa 1080
 ggttcttaac gccatcgaag acaatgggtt aaagaactca acattcacgt atttcacctc 1140
 tgaccatgga ggacatttag aggcaagaga tggacacagc cagttagggg gatggaacgg 1200
 aatttaciaa ggtgggaagg gcatgggagg atgggaaggt gggatccgag tgcccgggat 1260
 cttccactgg ccgggggtgc tcccggccgg ccgagtgatt ggagagccca cgagcctgat 1320
 ggacgtgttc cctactgtgg tccagctggt ggggtggcgag gtgccccagg acagggtgat 1380
 tgatggccac agcctgttac ccttgctgca gggagctgag gcacgctcgg cacatgagtt 1440
 cctgtttcat tactgtgggc agcatcttca cgcagcacgc tggcaccaga aggacagtgg 1500
 aagcgtctgg aaggttcatt acacgacccc gcagttccac cccgaggagc ggggcctgct 1560
 aacggccgag gcgtctgccc atgctgaatg gggaggcgtg acccatcaca gacccccctt 1620
 gctctttgac ctctccaggg accctccga ggcacggccc ctgacccccg actccgagcc 1680
 cctgtaccac gccgtgatag caagggtagg tgccgcggtg tcggagcatc ggcagaccct 1740
 gagtcctgtg cccagcagc tttccatgag caacatcctg tggaagccgt ggctgcagcc 1800
 gtgctgcgga catttccgt tctgttcatg ccacaggat ggggatggca cccctgaat 1860
 gccaggactg tgagagagga tccaggagag cctgactgcg ttgcaaacia aattctccaa 1920
 gcttggttct atcttcagtc cggaa 1945

<210> 21
 <211> 593
 <212> PRT
 <213> Homo sapiens
 <400> 21

Met Arg Ser Ala Ala Arg Arg Gly Arg Ala Ala Pro Ala Ala Arg Asp
 1 5 10 15

Ser Leu Pro Val Leu Leu Phe Leu Cys Leu Leu Leu Lys Thr Cys Glu
 20 25 30

Pro Lys Thr Ala Asn Ala Phe Lys Pro Asn Ile Leu Leu Ile Met Ala
35 40 45

Asp Asp Leu Gly Thr Gly Asp Leu Gly Cys Tyr Gly Asn Asn Thr Leu
50 55 60

Arg Thr Pro Asn Ile Asp Gln Leu Ala Glu Glu Gly Val Arg Leu Thr
65 70 75 80

Gln His Leu Ala Ala Ala Pro Leu Cys Thr Pro Ser Arg Ala Ala Phe
85 90 95

Leu Thr Gly Arg His Ser Phe Arg Ser Gly Met Asp Ala Ser Asn Gly
100 105 110

Tyr Arg Ala Leu Gln Trp Asn Ala Gly Ser Gly Gly Leu Pro Glu Asn
115 120 125

Glu Thr Thr Phe Ala Arg Ile Leu Gln Gln His Gly Tyr Ala Thr Gly
130 135 140

Leu Ile Gly Lys Trp His Gln Gly Val Asn Cys Ala Ser Arg Gly Asp
145 150 155 160

His Cys His His Pro Leu Asn His Gly Phe Asp Tyr Phe Tyr Gly Met
165 170 175

Pro Phe Thr Leu Thr Asn Asp Cys Asp Pro Gly Arg Pro Pro Glu Val
180 185 190

Asp Ala Ala Leu Arg Ala Gln Leu Trp Gly Tyr Thr Gln Phe Leu Ala
195 200 205

Leu Gly Ile Leu Thr Leu Ala Ala Gly Gln Thr Cys Gly Phe Phe Ser
210 215 220

Val Ser Ala Arg Ala Val Thr Gly Met Ala Gly Val Gly Cys Leu Phe
225 230 235 240

Phe Ile Ser Trp Tyr Ser Ser Phe Gly Phe Val Arg Arg Trp Asn Cys
245 250 255

Ile Leu Met Arg Asn His Asp Val Thr Glu Gln Pro Met Val Leu Glu
260 265 270

Lys Thr Ala Ser Leu Met Leu Lys Glu Ala Val Ser Tyr Ile Glu Arg
275 280 285

His Lys His Gly Pro Phe Leu Leu Phe Leu Ser Leu Leu His Val His
290 295 300

Ile Pro Leu Val Thr Thr Ser Ala Phe Leu Gly Lys Ser Gln His Gly
305 310 315 320

Leu Tyr Gly Asp Asn Val Glu Glu Met Asp Trp Leu Ile Gly Lys Val
325 330 335

Leu Asn Ala Ile Glu Asp Asn Gly Leu Lys Asn Ser Thr Phe Thr Tyr
340 345 350

Phe Thr Ser Asp His Gly Gly His Leu Glu Ala Arg Asp Gly His Ser
355 360 365

Gln Leu Gly Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly
370 375 380

Gly Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Phe His Trp Pro Gly
385 390 395 400

Val Leu Pro Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp
405 410 415

Val Phe Pro Thr Val Val Gln Leu Val Gly Gly Glu Val Pro Gln Asp
420 425 430

Arg Val Ile Asp Gly His Ser Leu Val Pro Leu Leu Gln Gly Ala Glu
435 440 445

Ala Arg Ser Ala His Glu Phe Leu Phe His Tyr Cys Gly Gln His Leu
450 455 460

His Ala Ala Arg Trp His Gln Lys Asp Ser Gly Ser Val Trp Lys Val
465 470 475 480

His Tyr Thr Thr Pro Gln Phe His Pro Glu Glu Arg Gly Leu Leu Thr
485 490 495

Ala Glu Ala Ser Ala His Ala Glu Trp Gly Gly Val Thr His His Arg
500 505 510

Pro Pro Leu Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Ala Arg Pro
515 520 525

Leu Thr Pro Asp Ser Glu Pro Leu Tyr His Ala Val Ile Ala Arg Val
530 535 540

Gly Ala Ala Val Ser Glu His Arg Gln Thr Leu Ser Pro Val Pro Gln
545 550 555 560

Gln Phe Ser Met Ser Asn Ile Leu Trp Lys Pro Trp Leu Gln Pro Cys
565 570 575

Cys Gly His Phe Pro Phe Cys Ser Cys His Glu Asp Gly Asp Gly Thr
580 585 590

Pro

<210> 22
<211> 1858
<212> DNA
<213> Homo sapiens

<400> 22
ccttcctctt cttgatcggg gattcaggaa ggagcccagg agcagaggaa gtagagagag 60
agacaacatg ttacatctgc accattcttg tttgtgtttc aggagctggc tgccagcgat 120

gctcgctgta ctgctaagtt tggcaccatc agcttccagc gacatttccg cctccccgacc 180
gaacatcctt cttctgatgg cggacgacct tggcattggg gacattgggt gctatggcaa 240
caacaccatg aggactccga atattgaccg ccttgacagag gacggcgtga agctgaccca 300
acacatctct gccgcatctt tgtgcacccc aagcagagcc gccttctca cgggcagata 360
ccctgtgcca tcagggatgg tttccagcat tggttaccgt gttcttcagt ggaccggagc 420
atctggaggt cttccaacaa atgagacaac ttttgcaaaa atactgaaag agaaaggcta 480
tgccactgga ctcatggaa aatggcatct gggcttcaac tgtgagtcag ccagtgatca 540
ttgccaccac cctctccatc atggccttga gcatttctac ggaatgcctt tctccttgat 600
gggtgattgc gcccgctggg aactctcaga gaagcgtgtc aacctggaac aaaaactcaa 660
cttctcttcc caagtctggg ccttggttgc cctcacactg gtagcaggga agctcacaca 720
cctgatcccc gtctcgtgga tgccggtcat ctggtcagcc ctttcggccg tctctctcct 780
cgcaagctcc tattttgtgg gtgctctgat tgtccatgcc gattgctttc tgatgagaaa 840
ccacaccatc acggagcagc ccattgtgctt ccaaagaacg acaccctta ttctgcagga 900
ggttgcgctc tttctcaaaa ggaataagca tgggcctttc ctctctttg tttcctttct 960
acacgttcac atccctctta tcactatgga gaacttctc gggaagagtc tccacgggct 1020
gtatggggac aacgtagagg agatggactg gatggtagga cggatccttg acactttgga 1080
cgtggagggg ttgagcaaca gcacctcat ttattttacg tcggatcacg gcggttcctt 1140
agagaatcaa cttggaaaca cccagtatgg tggctggaat ggaatttata aagggtgggaa 1200
gggcatggga ggatgggaag gtgggatccg cgtgcccggg atcttccgct ggcccggggt 1260
gtccccggcc ggccgagtga ttggcgagcc cagcagctgt atggacgtgt tccccaccgt 1320
ggtccggctg gcgggcggcg aggtgcccc aagacagagt attgacggcc aagaccttct 1380
gcccttgctc ctggggacag cccaacactc agaccacgag ttcctgatgc attattgtga 1440
gaggtttctg cagcgagcca ggtggcatca acgggacaga ggaacaatgt ggaaagtcca 1500
ctttgtgacg cctgtgttcc agccagaggg agccggtgcc tgctatggaa gaaaggtctg 1560
cccgtgcttt ggggaaaaag tagtccacca cgatccacct ttgctctttg acctctcaag 1620
agaccttct gagaccacaca tctcacacc agcctcagag cccgtgttct atcaggtgat 1680
ggaacgagtc cagcaggcgg tgtgggaaca ccagcggaca ctacagcccag ttcctctgca 1740
gctggacagg ctgggcaaca tctggagacc gtggctgcag ccctgctgtg gcccgttccc 1800
cctctgctgg tgccttaggg aagatgaccc acaataaatg tctgcagtga aaagctgg 1858

<210> 23
<211> 589
<212> PRT
<213> Homo sapiens

<400> 23

Met Leu His Leu His His Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
1 5 10 15

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
20 25 30

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu
35 40 45

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro
50 55 60

Asn Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile
65 70 75 80

Ser Ala Ala Ser Leu Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly
85 90 95

Arg Tyr Pro Val Arg Ser Gly Met Val Ser Ser Ile Gly Tyr Arg Val
100 105 110

Leu Gln Trp Thr Gly Ala Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr
115 120 125

Phe Ala Lys Ile Leu Lys Glu Lys Gly Tyr Ala Thr Gly Leu Ile Gly
130 135 140

Lys Trp His Leu Gly Leu Asn Cys Glu Ser Ala Ser Asp His Cys His
145 150 155 160

His Pro Leu His His Gly Phe Glu His Phe Tyr Gly Met Pro Phe Ser
165 170 175

Leu Met Gly Asp Cys Ala Arg Trp Glu Leu Ser Glu Lys Arg Val Asn
180 185 190

Leu Glu Gln Lys Leu Asn Phe Leu Phe Gln Val Leu Ala Leu Val Ala
195 200 205

Leu Thr Leu Val Ala Gly Lys Leu Thr His Leu Ile Pro Val Ser Trp
210 215 220

Met Pro Val Ile Trp Ser Ala Leu Ser Ala Val Leu Leu Leu Ala Ser
225 230 235 240

Ser Tyr Phe Val Gly Ala Leu Ile Val His Ala Asp Cys Phe Leu Met
245 250 255

Arg Asn His Thr Ile Thr Glu Gln Pro Met Cys Phe Gln Arg Thr Thr
260 265 270

Pro Leu Ile Leu Gln Glu Val Ala Ser Phe Leu Lys Arg Asn Lys His
275 280 285

Gly Pro Phe Leu Leu Phe Val Ser Phe Leu His Val His Ile Pro Leu
290 295 300

Ile Thr Met Glu Asn Phe Leu Gly Lys Ser Leu His Gly Leu Tyr Gly
305 310 315 320

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Arg Ile Leu Asp Thr
325 330 335

Leu Asp Val Glu Gly Leu Ser Asn Ser Thr Leu Ile Tyr Phe Thr Ser
340 345 350

Asp His Gly Gly Ser Leu Glu Asn Gln Leu Gly Asn Thr Gln Tyr Gly
355 360 365

Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu
370 375 380

Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Gly Val Leu Pro
385 390 395 400

Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp Val Phe Pro
405 410 415

Thr Val Val Arg Leu Ala Gly Gly Glu Val Pro Gln Asp Arg Val Ile
420 425 430

Asp Gly Gln Asp Leu Leu Pro Leu Leu Leu Gly Thr Ala Gln His Ser
435 440 445

Asp His Glu Phe Leu Met His Tyr Cys Glu Arg Phe Leu His Ala Ala
450 455 460

Arg Trp His Gln Arg Asp Arg Gly Thr Met Trp Lys Val His Phe Val
465 470 475 480

Thr Pro Val Phe Gln Pro Glu Gly Ala Gly Ala Cys Tyr Gly Arg Lys
485 490 495

Val Cys Pro Cys Phe Gly Glu Lys Val Val His His Asp Pro Pro Leu
500 505 510

Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Thr His Ile Leu Thr Pro
515 520 525

Ala Ser Glu Pro Val Phe Tyr Gln Val Met Glu Arg Val Gln Gln Ala
530 535 540

Val Trp Glu His Gln Arg Thr Leu Ser Pro Val Pro Leu Gln Leu Asp
545 550 555 560

Arg Leu Gly Asn Ile Trp Arg Pro Trp Leu Gln Pro Cys Cys Gly Pro
565 570 575

Phe Pro Leu Cys Trp Cys Leu Arg Glu Asp Asp Pro Gln
580 585

<210> 24
<211> 1996
<212> DNA
<213> Homo sapiens

<400> 24
gggttctgct cctagacatt agagagataa tacggctgat agacaacaag aaggatttcc 60
aagctgcaca atgaggccca ggagaccgtt ggtcttcatt tctttggtgt gtgcactctt 120
gaacacatgg ccagggcaca cagggtgcat gacgacaagg cctaattattg tcctaattcat 180
ggttgatgac ctgggtattg gagatctggg ctgctacggc aatgacacca tgaggacgcc 240
tcacatcgac cgccttgcca gggaaggcgt gcgactgact cagcacatct ctgccgcctc 300
cctctgcagc ccaagccggt ccgcgttctt gacgggaaga taccatccatcc gatcagggtat 360
ggtttctagt ggtaatatagac gtgtcatcca aaatcttgca gtccccgcag gcctccctct 420

taatgagaca acacttgcag ccttgctaaa gaagcaagga tacagcacgg ggcttatagg 480
 caaatggcac caaggcttga actgcgactc ccgaagtga cagtgccacc atccatataa 540
 ttatgggttt gactactact atggcatgcc gttcactctc gttgacagct gctggccgga 600
 cccctctcgt aacacggaat tagcctttga gagtcagctc tggctctgtg tgcagctagt 660
 tgccattgcc atcctcaccc taacctttgg gaagctgagc ggctgggtct ctgttccttg 720
 gtcctgac tctcctatga tctctgttat tttcctcttg ggctatgctt ggctctccag 780
 ccacacgtcc cctttatact gggactgcct cctcatgcgg gggcacgaga tcacggagca 840
 gcccatgaag gctgaacgag ctggatccat tatggtgaag gaagcgattt cctttttaga 900
 aaggcacagt aaggaaactt tccttctctt tttctccttt cttcacgtgc acacacctct 960
 cccaccacg gacgatttca ctggcaccag caagcatggc ttgtatgggg ataattgtgga 1020
 agagatggac tccatggtgg gcaagattct tgatgctatc gatgattttg gcctaaggaa 1080
 caacaccctt gtctacttta catcagatca cggagggcat ttggaagcta ggcgagggca 1140
 tgcccaactt ggtggatgga atggaatata caaaggtgga aaaggcatgg ggggctggga 1200
 aggtggaatc cgcgtcccag gaattgtccg atggcctgga aaggtaccag ctggacgggt 1260
 gattaaggaa cctacaagtt taatggatat ttaccaact gtcgcatcag tgtcaggagg 1320
 aagtctcctt caggacaggg tcattgacgg ccgagacctc atgcccttgc tgcagggcaa 1380
 cgtcaggcac tcggagcatg aatttctttt ccactactgt ggctcctacc tgcacgccgt 1440
 gcggtggatc cccaaggacg acagtgggtc agtttggaag gctcactatg tgaccccggt 1500
 attccagcca ccagcttctg gtggctgcta tgtcacctca ttatgcagat gtttcggaga 1560
 acaggttacc taccacaacc cccctctgct cttcgatctc tccagggacc cctcagagtc 1620
 cacaccctg acacctgcca cagagcccct ctatgatttt gtgattaaaa aggtggccaa 1680
 cgccctgaag gaacaccagg aaaccatcgt gcctgtgacc taccaactct cagaactgaa 1740
 tcagggcagg acgtggctga agccttgctg tggggtgttc ccattttgtc tgtgtgacaa 1800
 ggaagaggaa gtctctcagc ctcggggtcc taacgagaag agataattac aatcaggcta 1860
 ccagaggaag cctttggtcc taacgagaag agataattac aatcaggcta ccaaaggaag 1920
 cactaacttt ggtgctttca agttggcaag gagtgcattt aatagtcaat aaattcatct 1980
 accattccag attatt 1996

<210> 25
 <211> 591
 <212> PRT
 <213> Homo sapiens

<400> 25

Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys Ala Leu
 1 5 10 15

Leu Asn Thr Trp Pro Gly His Thr Gly Cys Met Thr Thr Arg Pro Asn
 20 25 30

Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly Cys
 35 40 45

Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala Arg
 50 55 60

Glu	Gly	Val	Arg	Leu	Thr	Gln	His	Ile	Ser	Ala	Ala	Ser	Leu	Cys	Ser	
65					70					75					80	
Pro	Ser	Arg	Ser	Ala	Phe	Leu	Thr	Gly	Arg	Tyr	Pro	Ile	Arg	Ser	Gly	
				85					90					95		
Met	Val	Ser	Ser	Gly	Asn	Arg	Arg	Val	Ile	Gln	Asn	Leu	Ala	Val	Pro	
			100					105					110			
Ala	Gly	Leu	Pro	Leu	Asn	Glu	Thr	Thr	Leu	Ala	Ala	Leu	Leu	Lys	Lys	
		115					120						125			
Gln	Gly	Tyr	Ser	Thr	Gly	Leu	Ile	Gly	Lys	Trp	His	Gln	Gly	Leu	Asn	
	130					135					140					
Cys	Asp	Ser	Arg	Ser	Asp	Gln	Cys	His	His	Pro	Tyr	Asn	Tyr	Gly	Phe	
145					150					155					160	
Asp	Tyr	Tyr	Tyr	Gly	Met	Pro	Phe	Thr	Leu	Val	Asp	Ser	Cys	Trp	Pro	
				165					170					175		
Asp	Pro	Ser	Arg	Asn	Thr	Glu	Leu	Ala	Phe	Glu	Ser	Gln	Leu	Trp	Leu	
			180					185					190			
Cys	Val	Gln	Leu	Val	Ala	Ile	Ala	Ile	Leu	Thr	Leu	Thr	Phe	Gly	Lys	
		195					200					205				
Leu	Ser	Gly	Trp	Val	Ser	Val	Pro	Trp	Leu	Leu	Ile	Phe	Ser	Met	Ile	
	210					215					220					
Leu	Phe	Ile	Phe	Leu	Leu	Gly	Tyr	Ala	Trp	Phe	Ser	Ser	His	Thr	Ser	
225					230					235					240	
Pro	Leu	Tyr	Trp	Asp	Cys	Leu	Leu	Met	Arg	Gly	His	Glu	Ile	Thr	Glu	
				245					250					255		
Gln	Pro	Met	Lys	Ala	Glu	Arg	Ala	Gly	Ser	Ile	Met	Val	Lys	Glu	Ala	
			260					265					270			
Ile	Ser	Phe	Leu	Glu	Arg	His	Ser	Lys	Glu	Thr	Phe	Leu	Leu	Phe	Phe	
		275					280					285				
Ser	Phe	Leu	His	Val	His	Thr	Pro	Leu	Pro	Thr	Thr	Asp	Asp	Phe	Thr	
	290					295					300					
Gly	Thr	Ser	Lys	His	Gly	Leu	Tyr	Gly	Asp	Asn	Val	Glu	Glu	Met	Asp	
305					310					315				320		
Ser	Met	Val	Gly	Lys	Ile	Leu	Asp	Ala	Ile	Asp	Asp	Phe	Gly	Leu	Arg	
				325					330					335		
Asn	Asn	Thr	Leu	Val	Tyr	Phe	Thr	Ser	Asp	His	Gly	Gly	His	Leu	Glu	
			340					345					350			
Ala	Arg	Arg	Gly	His	Ala	Gln	Leu	Gly	Gly	Trp	Asn	Gly	Ile	Tyr	Lys	
		355					360					365				
Gly	Gly	Lys	Gly	Met	Gly	Gly	Trp	Glu	Gly	Gly	Ile	Arg	Val	Pro	Gly	
	370					375					380					

Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys Glu
 385 390 395 400

Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser Gly
 405 410 415

Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met Pro
 420 425 430

Leu Leu Gln Gly Asn Val Arg His Ser Glu His Glu Phe Leu Phe His
 435 440 445

Tyr Cys Gly Ser Tyr Leu His Ala Val Arg Trp Ile Pro Lys Asp Asp
 450 455 460

Ser Gly Ser Val Trp Lys Ala His Tyr Val Thr Pro Val Phe Gln Pro
 465 470 475 480

Pro Ala Ser Gly Gly Cys Tyr Val Thr Ser Leu Cys Arg Cys Phe Gly
 485 490 495

Glu Gln Val Thr Tyr His Asn Pro Pro Leu Leu Phe Asp Leu Ser Arg
 500 505 510

Asp Pro Ser Glu Ser Thr Pro Leu Thr Pro Ala Thr Glu Pro Leu Tyr
 515 520 525

Asp Phe Val Ile Lys Lys Val Ala Asn Ala Leu Lys Glu His Gln Glu
 530 535 540

Thr Ile Val Pro Val Thr Tyr Gln Leu Ser Glu Leu Asn Gln Gly Arg
 545 550 555 560

Thr Trp Leu Lys Pro Cys Cys Gly Val Phe Pro Phe Cys Leu Cys Asp
 565 570 575

Lys Glu Glu Glu Val Ser Gln Pro Arg Gly Pro Asn Glu Lys Arg
 580 585 590

<210> 26
 <211> 1578
 <212> DNA
 <213> Homo sapiens

<400> 26
 atgggctggc tttttctaaa ggttttggtg gcgaggagtg gtttctcagg atttctttat 60
 cctcttggtg atttttgcat cagtgggaaa acaagaggac agaagccaaa ctttgtgatt 120
 attttggccg atgacatggg gtggggtgac ctgggagcaa actgggcaga aacaaaggac 180
 actgccaacc ttgataagat ggcttcggag ggaatgaggt ttgtggattt ccatgcagct 240
 gcctccacct gtcaccctc ccgggcttcc ttgctcaccg gccggcttgg ccttcgcaat 300
 ggagtcacac gcaactttgc agtcacttct gtgggaggcc ttccgctcaa cgagaccacc 360
 ttggcagagg tgctgcagca ggcgggttac gtcactggga taataggcaa atggcatctt 420
 ggacaccacg gctcttatca ccccaacttc cgtgggtttg attactactt tggaatccca 480
 tatagccatg atatgggctg tactgatact ccaggctaca accaccctcc ttgtccagcg 540

tgtccacagg gtgatggacc atcaaggaac cttcaaagag actgttacac tgacgtggcc 600
ctccctcttt atgaaaacct caacattgtg gagcagccgg tgaacttgag cagccttgcc 660
cagaagtatg ctgagaaaagc aaccagttc atccagcgtg caagcaccag cgggaggccc 720
ttcctgtctt atgtggctct ggcccacatg cacgtgccct tacctgtgac tcagctacca 780
gcagcgccac ggggcagaag cctgtatggt gcagggctct gggagatgga cagtctggtg 840
ggccagatca aggacaaagt tgaccacaca gtgaaggaaa acacattcct ctggtttaca 900
ggagacaatg gcccgtgggc tcagaagtgt gagctagcgg gcagtgtggg tcccttcact 960
ggattttggc aaactcgtca agggggaagt ccagccaagc agacgacctg ggaaggaggg 1020
caccgggtcc cagcactggc ttactggcct ggcagagttc cagttaatgt caccagcact 1080
gccttggttaa gcgtgctgga cttttttcca actgtggtag ccctggccca ggccagctta 1140
cctcaaggac ggcgctttga tgggtgtggac gtctccgagg tgctctttgg ccggtcacag 1200
cctgggcaca ggggtgctgt ccacccaac agcggggcag ctggagagtt tggagccctg 1260
cagactgtcc gcctggagcg ttacaaggcc ttctacatta ccggtggagc cagggcgtgt 1320
gatgggagca cggggcctga gctgcagcat aagtttcctc tgattttcaa cctggaagac 1380
gataccgcag aagctgtgcc cctagaaaga ggtggtgagg agtaccaggc tgtgctgccc 1440
gaggtcagaa aggttcttgc agacgtctc caagacattg ccaacgacaa catctccagc 1500
gcagattaca ctcaggaccc ttcaagtaact ccctgctgta atccctacca aattgcctgc 1560
cgctgtcaag ccgcataa 1578

<210> 27
<211> 525
<212> PRT
<213> Homo sapiens

<400> 27

Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser Phe Ser
1 5 10 15

Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
20 25 30

Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
35 40 45

Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
50 55 60

Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
65 70 75 80

Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
85 90 95

Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
100 105 110

Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
115 120 125

Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
130 135 140

Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
145 150 155 160

Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro
165 170 175

Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
180 185 190

Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
195 200 205

Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
210 215 220

Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
225 230 235 240

Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
245 250 255

Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
260 265 270

Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
275 280 285

His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly
290 295 300

Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr
305 310 315 320

Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr
325 330 335

Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg
340 345 350

Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile
355 360 365

Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg
370 375 380

Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln
385 390 395 400

Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu
405 410 415

Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr
420 425 430

Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu
435 440 445

Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu
450 455 460

Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro
465 470 475 480

Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp
485 490 495

Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys
500 505 510

Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala
515 520 525

<210> 28
<211> 4669
<212> DNA
<213> Homo sapiens

<400> 28
cgagaccgt cgctaatgaa tcttggggcc ggtgtcgggc cggggcggct tgatcggcaa 60
ctaggaaacc ccaggcgcag aggccaggag cgagggcagc gaggatcaga ggccaggcct 120
tcccggtgc cggcgctcct cggaggtcag ggcagatgag gaacatgact ctcccccttc 180
ggaggaggaa ggaagtcccc ctgccacctt atctctgctc ctctgcctcc tccctgttcc 240
cagagctttt tctctagaga agattttgaa ggcggctttt gtgctgacgg ccaccaccca 300
tcatctaaag aagataaact tggcaaatga catgcagggt cttcaaggca gaataattgc 360
agaaaatctt caaaggaccc tatctgcaga tgttctgaat acctctgaga atagagattg 420
attattcaac caggatacct aattcaagaa ctccagaaat caggagacgg agacattttg 480
tcagttttgc aacattggac caaatacaat gaagtattct tgctgtgctc tggttttggc 540
tgtcctgggc acagaattgc tgggaagcct ctgttcgact gtcagatccc cgaggttcag 600
aggacggata cagcaggaac gaaaaaacat ccgaccaac attattcttg tgcttaccga 660
tgatcaagat gtggagctgg ggtccctgca agtcatgaac aaaacgagaa agattatgga 720
acatgggggg gccaccttca tcaatgcctt tgtgactaca cccatgtgct gcccgtcacg 780
gtcctccatg ctcaccggga agtatgtgca caatcacaat gtctacacca acaacgagaa 840
ctgctcttcc cctcgtggc aggccatgca tgagcctcgg acttttgctg tatatcttaa 900
caacactggc tacagaacag ctttttttgg aaaatacctc aatgaatata atggcagcta 960
catccccctt ggggtggcag aatggcttgg attaatacaag aattctcgtc tctataatta 1020
cactgtttgt cgcaatggca tcaaagaaaa gcatggattt gattatgcaa aggactactt 1080
cacagactta atcactaacg agagcattaa ttacttcaaa atgtctaaga gaatgtatcc 1140
ccataggccc gttatgatgg tgatcagcca cgctgcgccc cacggccccg aggactcagc 1200
cccacagttt tctaaactgt accccaatgc ttcccaacac ataactccta gttataacta 1260
tgcaccaa atggataaac actggattat gcagtacaca ggaccaatgc tgcccatcca 1320
catggaattt acaaacattc tacagcgcaa aaggctccag actttgatgt cagtggatga 1380
ttctgtggag aggtgtgata acatgctcgt ggagacgggg gagctggaga atacttacat 1440
catttacacc gccgaccatg gttaccatat tgggcagttt ggactgggtca aggggaaatc 1500
catgccatat gactttgata ttcgtgtgcc tttttttatt cgtgggtccaa gtgtagaacc 1560

aggatcaata	gtccacaga	tcgttctcaa	cattgacttg	gccccacga	tcctggatat	1620
tgctgggctc	gacacacctc	ctgatgtgga	cggcaagtct	gtcctcaaac	ttctggaccc	1680
agaaaagcca	ggtaacagg	ttcgaacaaa	caagaaggcc	aaaatttggc	gtgatacatt	1740
cctagtggaa	agaggcaaat	ttctacgtaa	gaaggaagaa	tccagcaaga	atatccaaca	1800
gtcaaatcac	ttgccccaat	atgaacgggt	caaagaacta	tgccagcagg	ccaggtacca	1860
gacagcctgt	gaacaaccgg	ggcagaagt	gcaatgcatt	gaggatacat	ctggcaagct	1920
tcgaattcac	aagtgtaaag	gacccagtga	cctgctcaca	gtccggcaga	gcacgcggaa	1980
cctctacgct	cgcggttcc	atgacaaaga	caaagagtgc	agttgtaggg	agtctggtta	2040
ccgtgccagc	agaagccaaa	gaaagagtca	acggcaattc	ttgagaaacc	aggggactcc	2100
aaagtacaag	cccagatttg	tccatactcg	gcagacacgt	tccttgtccg	tcgaatttga	2160
aggtgaaata	tatgacataa	atctggaaga	agaagaagaa	ttgcaagtgt	tgcaaccaag	2220
aaacattgct	aagcgtcatg	atgaaggcca	caaggggcca	agagatctcc	aggcttccag	2280
tggtggcaac	aggggcagga	tgctggcaga	tagcagcaac	gccgtgggcc	cacctaccac	2340
tgcccgagt	acacacaagt	gttttattct	tcccaatgac	tctatccatt	gtgagagaga	2400
actgtaccaa	tcggccagag	cgtggaagga	ccataaggca	tacattgaca	aagagattga	2460
agctctgcaa	gataaaatta	agaatttaag	agaagtgaga	ggacatctga	agagaaggaa	2520
gcctgaggaa	tgtagctgca	gtaaacaaa	ctattacaat	aaagagaaag	gtgtaaaaaa	2580
gcaagagaaa	ttaaagagcc	atcttcaccc	attcaaggag	gctgctcagg	aagtagatag	2640
caaactgcaa	cttttcaagg	agaacaaccg	taggaggaag	aaggagagga	aggagaagag	2700
acggcagagg	aagggggaag	agtgcagcct	gcctggcctc	acttgcttca	cgcatgacaa	2760
caaccactgg	cagacagccc	cgttctggaa	cctgggatct	ttctgtgctt	gcacgagttc	2820
taacaataac	acctactgg	gtttgcgtac	agttaatgag	acgcataatt	ttcttttctg	2880
tgagtttgct	actggctttt	tggagtattt	tgatatgaat	acagatcctt	atcagctcac	2940
aaatacagt	cacacggtag	aacgaggcat	tttgaatcag	ctacacgtac	aactaatgga	3000
gctcagaagc	tgtaaggat	ataagcagt	caacccaaga	cctaagaatc	ttgatgttgg	3060
aaataaagat	ggaggaagct	atgacctaca	cagaggacag	ttatgggatg	gatgggaagg	3120
ttaatcagcc	ccgtctcact	gcagacatca	actggcaagg	cctagaggag	ctacacagt	3180
tgaatgaaaa	catctatgag	tacagacaaa	actacagact	tagtctggtg	gactggacta	3240
attacttgaa	ggatttagat	agagtatttg	cactgctgaa	gagtcactat	gagcaaaata	3300
aaacaaataa	gactcaaact	gctcaaagt	acgggttctt	ggttgtctct	gctgagcacg	3360
ctgtgtcaat	ggagatggcc	tctgctgact	cagatgaaga	cccaaggcat	aagggttggga	3420
aaacacctca	tttgaccttg	ccagctgacc	ttcaaaccct	gcatttgaac	cgaccaacat	3480
taagtccaga	gagtaaaact	gaatggaata	acgacattcc	agaagttaat	catttgaatt	3540
ctgaacactg	gagaaaaacc	gaaaaatgga	cggggcatga	agagactaat	catctggaaa	3600
ccgatttcag	tggcgatggc	atgacagagc	tagagctcgg	gccagcccc	aggctgcagc	3660
ccattcacag	gcacccgaaa	gaacttcccc	agtatggtgg	tcctggaaag	gacatttttg	3720
aagatcaact	atatcttctt	gtgcattccg	atggaatttc	agttcatcag	atgttcacca	3780
tggccaccgc	agaacaccga	agtaattcca	gcatagcggg	gaagatgttg	accaagggtg	3840
agaagaatca	cgaaaaggag	aagtcacagc	acctagaagg	cagcacctcc	tcttcaactt	3900

cctctgatta gatgaaactg ttaccttacc ctaaacacag tatttctttt taactttttt 3960
 atttgtaaac taataaaggt aatcacagcc accaacattc caagctaccc tgggtacctt 4020
 tgtgcagtag aagctagtga gcatgtgagc aagcgggtg caccaggaga ctcacgtta 4080
 taatttacta tctgccaaga gtagaaagaa aggctgggga tatttgggtt ggcttggtt 4140
 tgattttttg cttgtttgtt tgtttgtac taaaacagta ttatctttt aatatcgtag 4200
 ggacataagt atatacatgt tatccaatca agatggctag aatggcgcct ttctgagtgt 4260
 ctaaaacttg acacccttg taaatctttc aacacacttc cactgcctgc gtaatgaagt 4320
 tttgattcat ttttaaccac tggaattttt caatgccgtc attttcagtt agatgatttt 4380
 gcactttgag attaaaatgc catgtctatt tgattagtct tattttttta tttttacagg 4440
 cttatcagtc tcaactgttg ctgtcattgt gacaaagtca aataaacccc caaggacgac 4500
 acacagtatg gatcacatat tgtttgacat taagcttttg ccagaaaatg ttgcatgtgt 4560
 tttacctga cttgctaaaa tgcattagca gaaaggcatg gctaataatg ttggtggtga 4620
 aaataataaa ataagtaaat gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4669

<210> 29
 <211> 871
 <212> PRT
 <213> Homo sapiens

<400> 29

Met Lys Tyr Ser Cys Cys Ala Leu Val Leu Ala Val Leu Gly Thr Glu
 1 5 10 15

Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
 20 25 30

Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
 35 40 45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
 50 55 60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
 65 70 75 80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
 85 90 95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
 100 105 110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
 115 120 125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
 130 135 140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
 145 150 155 160

Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
 165 170 175

Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
180 185 190

Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
195 200 205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
210 215 220

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225 230 235 240

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
245 250 255

Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
260 265 270

Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
275 280 285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
290 295 300

Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305 310 315 320

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
325 330 335

Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
340 345 350

Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
355 360 365

Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
370 375 380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385 390 395 400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
405 410 415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
420 425 430

Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
435 440 445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
450 455 460

Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465 470 475 480

Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
485 490 495

Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
 500 505 510
 Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
 515 520 525
 Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
 530 535 540
 Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
 545 550 555 560
 Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
 565 570 575
 His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
 580 585 590
 Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
 595 600 605
 Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
 610 615 620
 Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
 625 630 635 640
 Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
 645 650 655
 Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
 660 665 670
 Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
 675 680 685
 Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
 690 695 700
 Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
 705 710 715 720
 Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
 725 730 735
 Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
 740 745 750
 His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
 755 760 765
 Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
 770 775 780
 Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
 785 790 795 800

Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
805 810 815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
820 825 830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
835 840 845

Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
850 855 860

Leu Trp Asp Gly Trp Glu Gly
865 870

<210> 30
<211> 4279
<212> DNA
<213> Homo sapiens

<400> 30
gggccatttc tggacaacag ctgctatattt cacttgagcc caagttaatt tctcggggag 60
ttctcggggcg cgcacaggca gctcgggttg ccctgcgatt gagctgcggg tcgcggccgg 120
cgccggcctc tccaatggca aatgtgtgtg gctggaggcg agcgcgaggc ttctggcaaa 180
ggcagtcgag tgtttgcaga cgggggagag tcctgtgaaa gcagataaaa gaaaacattt 240
attaacgtgt cattacgagg ggagcgcccg gccggggctg tcgcactccc cgcggaacat 300
ttggctccct ccagctccta gagaggagaa gaagaaagcg gaaaagaggc agattcacgt 360
cgtttccagc caagtggacc tgatcgatgg ccctcctgaa tttatcacga tatttgattt 420
attagcgatg ccccttggtt tgtgtgttac gcacacacac gtgcacacaa ggctctggct 480
cgcttccctc cctcgtttcc agctcctggg cgaatcccac atctgtttca actctccgcc 540
gagggcgagc aggagcgaga gtgtgtcgaa tctgcgagtg aagagggacg agggaaaaga 600
aaciaagcca cagacgcaac ttgagactcc cgcaccccaa aagaagcacc agatcagcaa 660
aaaaagaaga tgggcccccc gagcctcgtg ctgtgcttgc tgtccgcaac tgtgttctcc 720
ctgctgggtg gaagctcggc cttcctgtcg caccaccgcc tgaaaggcag gtttcagagg 780
gaccgcagga acatccgccc caacatcatc ctggtgctga cggacgacca ggatgtggag 840
ctgggttcca tgcaggtgat gaacaagacc cggcgcatca tggagcaggg cggggagcac 900
ttcatcaacg ccttcgtgac cacacccatg tgctgcccct cagctcctc catcctcacc 960
ggcaagtacg tccacaacca caacacctac accaacaatg agaactgctc ctgcacctcc 1020
tggcaggcac agcacgagag ccgcacctt gccgtgtacc tcaatagcac tggctaccgg 1080
acagctttct tcgggaagta tcttaatgaa tacaacggct cctacgtgcc acccggtgg 1140
aaggagtggg tcggactcct taaaaactcc cgcttttata actacacgct gtgtcggaac 1200
ggggtgaaag agaagcacgg ctccgactac tccaaggatt acctcacaga cctcatcacc 1260
aatgacagcg tgagcttctt ccgcacgtcc aagaagatgt acccgcacag gccagtcctc 1320
atggtcatca gccatgcagc ccccccaggg cctgaggatt cagccccaca atattcacgc 1380
ctcttcccaa acgcatctca gcacatcacg ccgagctaca actacgcgcc caaccgggac 1440
aaacactgga tcatgcgcta cacggggccc atgaagccca tccacatgga attcaccaac 1500
atgctccagc ggaagcgctt gcagaccctc atgtcgggtg acgactccat ggagacgatt 1560

tacaacatgc	tgggtgagac	gggagagctg	gacaacacgt	acatcgata	caccgcccac	1620
cacgggtacc	acatcgcca	gtttggcctg	gtgaaaggga	aatccatgcc	atatgagttt	1680
gacatcaggg	tcccgttcta	cgtgaggggc	cccaacgtgg	aagccggctg	tctgaatccc	1740
cacatcgtec	tcaacattga	cctggccccc	accatcctgg	acattgcagg	cctggacata	1800
cctgcggata	tggacgggaa	atccatcctc	aagctgctgg	acacggagcg	gccggtgaat	1860
cggtttcact	tgaaaaagaa	gatgaggggc	tggcgggact	ccttcttggt	ggagagagggc	1920
aagctgctac	acaagagaga	caatgacaag	gtggacgccc	aggaggagaa	ctttctgccc	1980
aagtaccagc	gtgtgaagga	cctgtgtcag	cgtgctgagt	accagacggc	gtgtgagcag	2040
ctgggacaga	agtggcagtg	tgtggaggac	gccacgggga	agctgaagct	gcataagtgc	2100
aagggcccca	tgcggctggg	cggcagcaga	gccctctcca	acctcgtgcc	caagtactac	2160
gggcagggca	gcgaggcctg	cacctgtgac	agcggggact	acaagctcag	cctggccgga	2220
cgccggaaaa	aactcttcaa	gaagaagtac	aaggccagct	atgtccgcag	tcgctccatc	2280
cgctcagtg	ccatcgaggt	ggacggcagg	gtgtaccacg	taggcctggg	tgatgccgcc	2340
cagccccgaa	acctaccaa	gcggcactgg	ccaggggccc	ctgaggacca	agatgacaag	2400
gatggtgggg	acttcagtg	cactggaggc	cttcccact	actcagccgc	caacccatt	2460
aaagtgcac	atcggtgcta	cactctagag	aacgacacag	tccagtgtga	cctggacctg	2520
tacaagtccc	tgcaggcctg	gaaagaccac	aagctgcaca	tcgaccacga	gattgaaacc	2580
ctgcagaaca	aaattaagaa	cctgagggaa	gtccgaggtc	acctgaagaa	aaagcggcca	2640
gaagaatgtg	actgtcacia	aatcagctac	cacaccagc	acaaaggccg	cctcaagcac	2700
agaggctcca	gtctgcatcc	tttcaggaag	ggcctgcaag	agaaggacaa	ggtgtggctg	2760
ttgcgggagc	agaagcgcaa	gaagaaactc	cgcaagctgc	tcaagcgcc	gcagaacaac	2820
gacacgtgca	gcatgccagg	cctcactgtc	ttcaccacg	acaaccagca	ctggcagacg	2880
gcgcctttct	ggacactggg	gcctttctgt	gcctgcacca	gcgccaacaa	taacacgtac	2940
tgggtgcatga	ggaccatcaa	tgagactcac	aatttcctct	tctgtgaatt	tgcaactggc	3000
ttcctagagt	actttgatct	caacacagac	ccctaccagc	tgatgaatgc	agtgaacaca	3060
ctggacaggg	atgtcctcaa	ccagctacac	gtacagctca	tggagctgag	gagctgcaag	3120
ggttacaagc	agtgtaaccc	cggactcga	aacatggacc	tgggacttaa	agatggagga	3180
agctatgagc	aatacaggca	gtttcagcgt	cgaaagtggc	cagaaatgaa	gagaccttct	3240
tccaaatcac	tgggacaact	gtgggaaggc	tgggaagggt	aagaaacaac	agaggtggac	3300
ctccaaaaac	atagaggcat	cacctgactg	cacaggcaat	gaaaaaccat	gtgggtgatt	3360
tccagcagac	ctgtgctatt	ggccaggagg	cctgagaaa	caagcacgca	ctctcagtca	3420
acatgacaga	ttctggagga	taaccagcag	gagcagagat	aacttcagga	agtccatttt	3480
tgcctctgct	tttcttttgg	attatacctc	accagctgca	caaaatgcat	tttttctgat	3540
caaaaagtca	ccactaaccc	tccccagaa	gctcacaaa	gaaaacggag	agagcgagcg	3600
agagagat	ccttggaat	ttctcccaag	ggcgaaagtc	attggaattt	ttaaatcata	3660
ggggaaaagc	agtccgtgtc	taaatcctct	tattcttttg	gtttgtcaca	aagaaggaa	3720
taagaagcag	gacagaggca	acgtggagag	gctgaaaaca	gtgcagagac	gtttgacaat	3780
gagtcagtag	cacaaaagag	atgacattta	cctagcatat	aaacctgggt	tgccctctgaa	3840
gaaactgcct	tcattgtata	tatgtgacta	tttacatgta	atcaacatgg	gaacttttag	3900

gggaacctaa taagaaatcc caattttcag gagtgggtgt gtcaataaac gctctgtggc 3960
cagtgtaaaa gaaaaaaaaa aaaaattgtg gacatttctg ttctgtcca gataccattt 4020
ctcctagtagt ttctttgtta tgtcccagaa ctgatgtttt ttttttaagg tactgaaaag 4080
aatgaagtt gatgtatgtc ccaagttttg atgaaactgt atttgtaaaa aaaattttgt 4140
agtttaagta ttgtcataca gtgttcaaaa cccagccaa tgaccagcag ttggtatgaa 4200
gaacctttga cattttgtaa aaggccattt cttggggaaa aaaaaaaaaa aaaaaaaaaa 4260
aaaaaaaaaa aaaaaaaaaa 4279

<210> 31
<211> 870
<212> PRT
<213> Homo sapiens

<400> 31

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
1 5 10 15

Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Leu Lys
20 25 30

Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu
35 40 45

Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met
50 55 60

Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Ala His Phe Ile Asn
65 70 75 80

Ala Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu
85 90 95

Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn
100 105 110

Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala
115 120 125

Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr
130 135 140

Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp
145 150 155 160

Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg
165 170 175

Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu
180 185 190

Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys
195 200 205

Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala
210 215 220

Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
 225 230 235 240

Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro
 245 250 255

Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His
 260 265 270

Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met
 275 280 285

Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr
 290 295 300

Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr
 305 310 315 320

His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu
 325 330 335

Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala
 340 345 350

Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr
 355 360 365

Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys
 370 375 380

Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His
 385 390 395 400

Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg
 405 410 415

Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu
 420 425 430

Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg
 435 440 445

Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys
 450 455 460

Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro
 465 470 475 480

Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr
 485 490 495

Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys
 500 505 510

Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys
 515 520 525

Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val
 530 535 540

Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg
545 550 555 560

Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp
565 570 575

Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser
580 585 590

Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn
595 600 605

Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp
610 615 620

Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn
625 630 635 640

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg
645 650 655

Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys
660 665 670

Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly
675 680 685

Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys
690 695 700

Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
705 710 715 720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln
725 730 735

Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala
740 745 750

Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn
755 760 765

Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu
770 775 780

Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg
785 790 795 800

Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys
805 810 815

Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly
820 825 830

Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg
835 840 845

Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu
850 855 860

Trp Glu Gly Trp Glu Gly
865 870

<210> 32
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(1)
<223> Leu OR Val

<220>
<221> misc_feature
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (2)..(2)
<223> Cys OR Ser

<220>
<221> VARIANT
<222> (3)..(3)
<223> Any Amino Acid

<400> 32

Xaa Xaa Xaa Pro Ser Arg
1 5

<210> 33
<211> 23
<212> PRT
<213> Artificial

<220>
<223> Sequence derived from human Arylsulfatase A

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> synthetic FGly formation substrate; primary sequence from human
Arylsulfatase A

<400> 33

Met Thr Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala
1 5 10 15

Ala Leu Leu Thr Gly Arg Ser
20

<210> 34
<211> 16
<212> PRT
<213> Artificial

<220>
<223> a variant of the ASA65-80 peptide, in which residues Cys69, Pro71
and Arg73, critical for FGly formation, were scrambled

<220>
<221> MISC_FEATURE
<222> (1)..(16)

<223> scrambled oligopeptide

<400> 34

Pro Val Ser Leu Pro Thr Arg Ser Cys Ala Ala Leu Leu Thr Gly Arg
1 5 10 15

<210> 35

<211> 16

<212> PRT

<213> Artificial

<220>

<223> a variant of the ASA65-80 peptide, in which the Cys69 was
replaced by a Serine

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> Ser69 oligopeptide

<400> 35

Pro Val Ser Leu Ser Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg
1 5 10 15

<210> 36

<211> 19

<212> DNA

<213> Artificial

<220>

<223> human FGE-specific PCR primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> human FGE-specific PCR primer 1199nc

<400> 36

ccaatgtagg tcagacacg

19

<210> 37

<211> 16

<212> DNA

<213> Artificial

<220>

<223> human FGE-specific PCR primer

<220>

<221> misc_feature

<222> (1)..(16)

<223> human FGE-specific forward PCR primer 1c

<400> 37

acatggcccg cgggac

16

<210> 38

<211> 19

<212> DNA

<213> Artificial

<220>

<223> human FGE-specific PCR primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> human FGE-specific reverse PCR primer 1182c

<400> 38
cgactgctcc ttggactgg 19

<210> 39
<211> 24
<212> DNA
<213> Artificial

<220>
<223> human FGE-specific PCR primer

<220>
<221> misc_feature
<222> (1)..(24)
<223> human 5' -FGE-specific PCR primer containing EcoRI

<400> 39
ggaattcggg acaacatggc tgcg 24

<210> 40
<211> 54
<212> DNA
<213> Artificial

<220>
<223> HA-specific primer

<220>
<221> misc_feature
<222> (1)..(54)
<223> HA-specific primer

<400> 40
cccaagctta tgcgtagtca ggcacatcat acggatagtc catggtgggc aggc 54

<210> 41
<211> 57
<212> DNA
<213> Artificial

<220>
<223> c-myc -specific primer

<220>
<221> misc_feature
<222> (1)..(57)
<223> c-myc -specific primer

<400> 41
cccaagctta caggtcttct tcagaaatca gcttttggtc gtccatggtg ggcaggc 57

<210> 42
<211> 54
<212> DNA
<213> Artificial

<220>
<223> RGS-His6 - specific primer

<220>
<221> misc_feature
<222> (1)..(54)
<223> RGS-His6 - specific primer

<400> 42
cccaagctta gtgatggtga tggatgatgcg atcctctgtc catggtgggc aggc 54

<210> 43

<211> 15
<212> PRT
<213> Artificial

<220>
<223> tryptic oligopeptide from a human FGE preparation

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> tryptic oligopeptide from a human FGE preparation

<400> 43

Ser Gln Asn Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly Phe Arg
1 5 10 15

<210> 44
<211> 19
<212> PRT
<213> Artificial

<220>
<223> tryptic oligopeptide from a human FGE preparation

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> tryptic oligopeptide from a human FGE preparation

<400> 44

Met Val Pro Ile Pro Ala Gly Val Phe Thr Met Gly Thr Asp Asp Pro
1 5 10 15

Gln Ile Lys

<210> 45
<211> 906
<212> DNA
<213> Homo sapiens

<400> 45
atggccccggc atgggttacc gctgctgccc ctgctgtcgc tcctggtcgg cgcggtggctc 60
aagctaggaa atggacaggc tactagcatg gtccaactgc aggggtgggag attcctgatg 120
ggaacaaatt ctccagacag cagagatggt gaagggcctg tgcggggaggc gacagtgaaa 180
ccctttgcca tcgacatatt tcctgtcacc aacaaagatt tcagggattt tgtcagggag 240
aaaaagtatc ggacagaagc tgagatgttt ggatggagct ttgtctttga ggactttgtc 300
tctgatgagc tgagaaacaa agccacccag ccaatgaagt ctgtactctg gtggcttcca 360
gtggaaaagg cattttggag gcagcctgca ggtcctggct ctggcatccg agagagactg 420
gagcaccagc tgttacacgt gagctggaat gacgcccgtg cctactgtgc ttggcgggga 480
aaacgactgc ccacggagga agagtgggag tttgccgccc gagggggcctt gaaggggtcaa 540
gtttacccat gggggaactg gttccagcca aaccgcacca acctgtggca gggaaagttc 600
cccaaggagg acaaaactga ggatggcttc catggagtct cccagtgaa tgctttcccc 660
gccagaaca actacgggct ctatgacctc ctggggaacg tgtgggagtg gacagcatca 720
ccgtaccagg ctgctgagca ggacatgcgc gtcctccggg gggcatcctg gatcgacaca 780
gctgatggct ctgccaatca cggggcccgg gtcaccacca ggatgggcaa cactccagat 840
tcagcctcag acaacctcgg tttccgctgt gctgcagacg caggccggcc gccaggggag 900

ctgtaa

906

<210> 46
 <211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46

Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu	Val
1				5					10					15	
Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val	Gln
			20					25					30		
Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser	Arg
		35					40					45			
Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala	Ile
	50					55					60				
Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg	Glu
65					70				75						80
Lys	Lys	Tyr	Arg	Thr	Glu	Ala	Glu	Met	Phe	Gly	Trp	Ser	Phe	Val	Phe
				85					90					95	
Glu	Asp	Phe	Val	Ser	Asp	Glu	Leu	Arg	Asn	Lys	Ala	Thr	Gln	Pro	Met
			100					105					110		
Lys	Ser	Val	Leu	Trp	Trp	Leu	Pro	Val	Glu	Lys	Ala	Phe	Trp	Arg	Gln
		115					120						125		
Pro	Ala	Gly	Pro	Gly	Ser	Gly	Ile	Arg	Glu	Arg	Leu	Glu	His	Pro	Val
		130				135					140				
Leu	His	Val	Ser	Trp	Asn	Asp	Ala	Arg	Ala	Tyr	Cys	Ala	Trp	Arg	Gly
145					150					155					160
Lys	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Trp	Glu	Phe	Ala	Ala	Arg	Gly	Gly
				165					170					175	
Leu	Lys	Gly	Gln	Val	Tyr	Pro	Trp	Gly	Asn	Trp	Phe	Gln	Pro	Asn	Arg
			180					185					190		
Thr	Asn	Leu	Trp	Gln	Gly	Lys	Phe	Pro	Lys	Gly	Asp	Lys	Ala	Glu	Asp
		195					200					205			
Gly	Phe	His	Gly	Val	Ser	Pro	Val	Asn	Ala	Phe	Pro	Ala	Gln	Asn	Asn
	210					215					220				
Tyr	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Asn	Val	Trp	Glu	Trp	Thr	Ala	Ser
225					230					235					240
Pro	Tyr	Gln	Ala	Ala	Glu	Gln	Asp	Met	Arg	Val	Leu	Arg	Gly	Ala	Ser
			245						250					255	
Trp	Ile	Asp	Thr	Ala	Asp	Gly	Ser	Ala	Asn	His	Arg	Ala	Arg	Val	Thr
			260					265					270		

Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe
275 280 285

Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu
290 295 300

<210> 47
<211> 927
<212> DNA
<213> Mus musculus

<400> 47
atgcgctctg agttctggtt ccccagcatg ggttccttgc tccctccggt gttgctgctg 60
aggctcctgt cctgccccag gcttcagcta ggacatgcc aggatcctgc catggtgcat 120
ctgccagggtg gccggtttct gatggggaca gacgctccag atggcagaga cggatgaaggg 180
cctgccccggg aagtgcagct aaaacccttt gccatcgaca tatttccagt caccaataaa 240
gacttcaggg agtttgtcag ggagaagaag taccagactg aagccgaggc attcgggtgg 300
agcttcgtct ttgaggattt tgtctcccct gagctcagaa agcaagaaaa tctgatgccg 360
gctgttcaact ggtggcagcc agtgccaaag gcatttttga ggcagcctgc aggtccccggc 420
tctggcatcc gagagaaact ggagcttccc gtggtacacg tgagctggaa cgacgctggt 480
gcttactgct catggcgggg gagacgcttg cccacagaag aggagtggga gtttgcagcc 540
cgaggggggt tgaagggtca ggtttatcca tgggggaacc ggttccagcc aaaccgcacc 600
aacttatggc agggaaagtt ccccaaaggt gacaaagctg aagatggttt tcatggactg 660
tcaccagtga acgctttccc cccacagaac aactacggac tgtatgacct catgggcaat 720
gtgtgggagt ggacagcgct cacataccaa cctgctggcc aggacatgct tgcctccgg 780
ggggcatcat gcatcgacac cgcagacggc tctgctaata acagggctcg ggtcaccacc 840
aggatgggaa aactccaga ctcagcctca gacaacctgg gcttccgctg cgctccagt 900
gcaggccgac cgaaggagga cctgtga 927

<210> 48
<211> 308
<212> PRT
<213> Mus musculus

<400> 48

Met Arg Ser Glu Phe Trp Phe Pro Ser Met Gly Ser Leu Leu Pro Pro
1 5 10 15

Val Leu Leu Leu Arg Leu Leu Ser Cys Pro Arg Leu Gln Leu Gly His
20 25 30

Ala Gln Asp Pro Ala Met Val His Leu Pro Gly Gly Arg Phe Leu Met
35 40 45

Gly Thr Asp Ala Pro Asp Gly Arg Asp Gly Glu Gly Pro Ala Arg Glu
50 55 60

Val Thr Val Lys Pro Phe Ala Ile Asp Ile Phe Pro Val Thr Asn Lys
65 70 75 80

Asp Phe Arg Glu Phe Val Arg Glu Lys Lys Tyr Gln Thr Glu Ala Glu
85 90 95

Ala Phe Gly Trp Ser Phe Val Phe Glu Asp Phe Val Ser Pro Glu Leu
100 105 110

Arg Lys Gln Glu Asn Leu Met Pro Ala Val His Trp Trp Gln Pro Val
115 120 125

Pro Lys Ala Phe Trp Arg Gln Pro Ala Gly Pro Gly Ser Gly Ile Arg
130 135 140

Glu Lys Leu Glu Leu Pro Val Val His Val Ser Trp Asn Asp Ala Gly
145 150 155 160

Ala Tyr Cys Ala Trp Arg Gly Arg Arg Leu Pro Thr Glu Glu Glu Trp
165 170 175

Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly Gln Val Tyr Pro Trp Gly
180 185 190

Asn Arg Phe Gln Pro Asn Arg Thr Asn Leu Trp Gln Gly Lys Phe Pro
195 200 205

Lys Gly Asp Lys Ala Glu Asp Gly Phe His Gly Leu Ser Pro Val Asn
210 215 220

Ala Phe Pro Pro Gln Asn Asn Tyr Gly Leu Tyr Asp Leu Met Gly Asn
225 230 235 240

Val Trp Glu Trp Thr Ala Ser Thr Tyr Gln Pro Ala Gly Gln Asp Met
245 250 255

Arg Val Leu Arg Gly Ala Ser Trp Ile Asp Thr Ala Asp Gly Ser Ala
260 265 270

Asn His Arg Ala Arg Val Thr Thr Arg Met Gly Asn Thr Pro Asp Ser
275 280 285

Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala Ser Ser Ala Gly Arg Pro
290 295 300

Lys Glu Asp Leu
305

<210> 49
<211> 855
<212> DNA
<213> Mus musculus

<400> 49
atgggtcccca ttcctgctgg agtattcaca atgggcactg atgacacctca gatcaggcag 60
gatggagaag ccctgccag gagagtcact gttgatggct tttacatgga cgcctatgaa 120
gtcagcaatg cggattttga gaagtttgtg aactcgactg gctatttgac agaggctgag 180
aagtttgagg actctttcgt ctttgaaggc atgttgagcg agcaagtga aacgcatatc 240
caccaggcag ttgcagctgc tccatggtgg ttgcctgtca agggagctaa ttggagacac 300
ccagagggtc cggactccag tattctgcac aggtcaaadc atccggttct ccatgtttcc 360
tggaacgatg ctgttgacct ctgcacatgg gctgggaaga ggttgacctac tgaggcagag 420
tggaataca gctgtagagg aggcctgcag aacaggcttt tccctgggg caacaaactg 480

cagcccaaag gacagcatta tgccaacatc tggcagggca agtttctgt gagcaacact 540
 ggcgaggatg gcttccaagg aactgcccc gttgatgcct ttcctccaa tggctatggc 600
 ttatacaaca tagtggggaa tgtgtgggag tggacctcag actggtggac tgttcacat 660
 tctgttgagg aaacgttcaa cccaaagggc cccacttctg ggaaagaccg agtgaagaag 720
 ggtggatcct acatgtgcca taagtcctat tgctataggt accgctgtgc agctcgaagc 780
 cagaacacac cagatagctc tgcattcaac ctgggattcc gatgtgcagc cgaccacctg 840
 cccaccgcag actga 855

<210> 50
 <211> 284
 <212> PRT
 <213> Mus musculus

<400> 50

Met Val Pro Ile Pro Ala Gly Val Phe Thr Met Gly Thr Asp Asp Pro
 1 5 10 15

Gln Ile Arg Gln Asp Gly Glu Ala Pro Ala Arg Arg Val Thr Val Asp
 20 25 30

Gly Phe Tyr Met Asp Ala Tyr Glu Val Ser Asn Ala Asp Phe Glu Lys
 35 40 45

Phe Val Asn Ser Thr Gly Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp
 50 55 60

Ser Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr His Ile
 65 70 75 80

His Gln Ala Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly Ala
 85 90 95

Asn Trp Arg His Pro Glu Gly Pro Asp Ser Ser Ile Leu His Arg Ser
 100 105 110

Asn His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr Cys
 115 120 125

Thr Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser
 130 135 140

Cys Arg Gly Gly Leu Gln Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu
 145 150 155 160

Gln Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Lys Phe Pro
 165 170 175

Val Ser Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val Asp
 180 185 190

Ala Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn Val
 195 200 205

Trp Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu Glu
 210 215 220

Thr Phe Asn Pro Lys Gly Pro Thr Ser Gly Lys Asp Arg Val Lys Lys
225 230 235 240

Gly Gly Ser Tyr Met Cys His Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys
245 250 255

Ala Ala Arg Ser Gln Asn Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly
260 265 270

Phe Arg Cys Ala Ala Asp His Leu Pro Thr Ala Asp
275 280

<210> 51
<211> 1011
<212> DNA
<213> Drosophila melanogaster

<400> 51
atgacaacaa ttatattagt cctctttatt tggatagttt tattcaatga cgtatccagc 60
gactgtggct gccaaaagct cgaccggaag gccccggata tgccgtccat ttccggacaa 120
gtgtgccagc aacgagcaca ggggtgcacac agccactacc gggattacta tggcgaactg 180
gagccaaata ttgcggacat gtcactgctt cggggaggca cggtttacat ggggtactgac 240
aaaccgcact ttccggccga ccgcgaggct ccggaacggc aggtgaagct gaatgacttc 300
tacatcgaca agtatgaggt ttccaacgaa gcctttgcga agtttgttct gcacactaac 360
tacaccacgg aggttgagcg atatggcgac agttttctgt ttaagagcct ttgagccca 420
ttggagcaga agaacctaga ggacttccga gtggcgagcg ctgtctggtg gtacaaagtg 480
gccggcgtga actggcgaca tccaaatggc gtggacagcg atatagacca cttaggccga 540
caccggtag tgcacgtatc gtggcgcgac gctgtggagt actgtaagtg ggccggcaag 600
cggttgccca gcgaggcgga gtgggaggcg gcttgcaggg gcggcaagga gcgcaaactg 660
tttcctgagg gcaacaagct gatgccaagg aatgaacatt ggctgaacat ctggcaggga 720
gactttcccg atggcaacct ggctgaagat gggtttgagt acaccagccc cgtggatgcc 780
ttccgacaga atatttacga cctgcacaac atggtgggca acgtctggga gtggacggca 840
gatctgtggg acgtaaatga cgtagcgat aatccaaatc gggtaagaa gggcggttct 900
tatctgtgtc acaagtccta ctgtacagg tacaggtgcg cggcacgctc gcagaacaca 960
gaagacagtt cagccggtaa cctgggtttt cgggtgcgca agaatgcgtg a 1011

<210> 52
<211> 336
<212> PRT
<213> Drosophila melanogaster

<400> 52

Met Thr Thr Ile Ile Leu Val Leu Phe Ile Trp Ile Val Leu Phe Asn
1 5 10 15

Asp Val Ser Ser Asp Cys Gly Cys Gln Lys Leu Asp Arg Lys Ala Pro
20 25 30

Asp Met Pro Ser Ile Ser Gly Gln Val Cys Gln Gln Arg Ala Gln Gly
35 40 45

Ala His Ser His Tyr Arg Asp Tyr Tyr Gly Glu Leu Glu Pro Asn Ile

50

55

60

Ala Asp Met Ser Leu Leu Pro Gly Gly Thr Val Tyr Met Gly Thr Asp
65 70 75 80

Lys Pro His Phe Pro Ala Asp Arg Glu Ala Pro Glu Arg Gln Val Lys
85 90 95

Leu Asn Asp Phe Tyr Ile Asp Lys Tyr Glu Val Ser Asn Glu Ala Phe
100 105 110

Ala Lys Phe Val Leu His Thr Asn Tyr Thr Thr Glu Ala Glu Arg Tyr
115 120 125

Gly Asp Ser Phe Leu Phe Lys Ser Leu Leu Ser Pro Leu Glu Gln Lys
130 135 140

Asn Leu Glu Asp Phe Arg Val Ala Ser Ala Val Trp Trp Tyr Lys Val
145 150 155 160

Ala Gly Val Asn Trp Arg His Pro Asn Gly Val Asp Ser Asp Ile Asp
165 170 175

His Leu Gly Arg His Pro Val Val His Val Ser Trp Arg Asp Ala Val
180 185 190

Glu Tyr Cys Lys Trp Ala Gly Lys Arg Leu Pro Ser Glu Ala Glu Trp
195 200 205

Glu Ala Ala Cys Arg Gly Gly Lys Glu Arg Lys Leu Phe Pro Trp Gly
210 215 220

Asn Lys Leu Met Pro Arg Asn Glu His Trp Leu Asn Ile Trp Gln Gly
225 230 235 240

Asp Phe Pro Asp Gly Asn Leu Ala Glu Asp Gly Phe Glu Tyr Thr Ser
245 250 255

Pro Val Asp Ala Phe Arg Gln Asn Ile Tyr Asp Leu His Asn Met Val
260 265 270

Gly Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Val Asn Asp Val
275 280 285

Ser Asp Asn Pro Asn Arg Val Lys Lys Gly Gly Ser Tyr Leu Cys His
290 295 300

Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn Thr
305 310 315 320

Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe Arg Cys Ala Lys Asn Ala
325 330 335

<210> 53
<211> 870
<212> DNA
<213> Anopheles gambiae

<400> 53
ccggagagct tgctcgatct ggtggaacat tccaagcggc tcgaagacat ggccttattc

60

```

ccaggaggtg aatatgtaat cggcacaaat gaacctatct tcgtcaagga tcgcgaatca 120
ccggccccggc ccgcgacgat ccgcgacttt tacctcgacc agtacgaagt ctccaacgca 180
cagttcaagg cattcgtcga ccagacgggc tacgtcacgg aggcggaaaa gtttggcgac 240
agcttcgtct tccagcagct gctcagcgaa ccggtgcgcc agcagtacga agatttcgcg 300
gtggcggcgg cgccctggtg gtacaaggta cgtggagcct cctggcagca tccggaaggt 360
gatgtgtcac gtgatataag cgaccgattg gaccatccgg tgggtgcacgt gtcctggaac 420
gatgcggtcg cgtactgcgc ctggaaaggg aagcgcctgc cgacggaagc ggaatgggaa 480
gcggcctgcc ggggcggtcg caagcagaag ctgttcccct ggggtaacaa gctgatgccg 540
aaggagcagc acatgatgaa catatggcag ggcgagttcc cggacagcaa tctgaaggag 600
gatggctacg agaccacctg cccggtgacg tccttcgcc agaaccggtt cgagctgtac 660
aacatcgttg gcaacgtgtg ggagtggacg gcggatcttt gggacgcgaa ggatgcggcc 720
atcgagcgca agccgggcag cgatccaccg aatcgggtga aaaaggggtg ctcatacctg 780
tgtcacgaat cgtactgcta tcgctatcgc tgtgcggctc gatcgagaa caccgaggac 840
agttcggcgg gcaatctggg cttccggtgc 870

```

```

<210> 54
<211> 290
<212> PRT
<213> Anopheles gambiae

```

```

<400> 54

```

```

Pro Glu Ser Leu Leu Asp Leu Val Glu His Ser Lys Arg Phe Glu Asp
1           5           10           15

```

```

Met Ser Leu Ile Pro Gly Gly Glu Tyr Val Ile Gly Thr Asn Glu Pro
20           25           30

```

```

Ile Phe Val Lys Asp Arg Glu Ser Pro Ala Arg Pro Ala Thr Ile Arg
35           40           45

```

```

Asp Phe Tyr Leu Asp Gln Tyr Glu Val Ser Asn Ala Gln Phe Lys Ala
50           55           60

```

```

Phe Val Asp Gln Thr Gly Tyr Val Thr Glu Ala Glu Lys Phe Gly Asp
65           70           75           80

```

```

Ser Phe Val Phe Gln Gln Leu Leu Ser Glu Pro Val Arg Gln Gln Tyr
85           90           95

```

```

Glu Asp Phe Arg Val Ala Ala Ala Pro Trp Trp Tyr Lys Val Arg Gly
100          105          110

```

```

Ala Ser Trp Gln His Pro Glu Gly Asp Val Ser Arg Asp Ile Ser Asp
115          120          125

```

```

Arg Leu Asp His Pro Val Val His Val Ser Trp Asn Asp Ala Val Ala
130          135          140

```

```

Tyr Cys Ala Trp Lys Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu
145          150          155          160

```

```

Ala Ala Cys Arg Gly Gly Arg Lys Gln Lys Leu Phe Pro Trp Gly Asn

```

165

170

175

Lys Leu Met Pro Lys Glu Gln His Met Met Asn Ile Trp Gln Gly Glu
180 185 190

Phe Pro Asp Ser Asn Leu Lys Glu Asp Gly Tyr Glu Thr Thr Cys Pro
195 200 205

Val Thr Ser Phe Arg Gln Asn Pro Phe Glu Leu Tyr Asn Ile Val Gly
210 215 220

Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Ala Lys Asp Ala Ala
225 230 235 240

Ile Glu Arg Lys Pro Gly Ser Asp Pro Pro Asn Arg Val Lys Lys Gly
245 250 255

Gly Ser Tyr Leu Cys His Glu Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala
260 265 270

Ala Arg Ser Gln Asn Thr Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe
275 280 285

Arg Cys
290

<210> 55
<211> 945
<212> DNA
<213> Streptomyces coelicolor

<400> 55
gtggccgtgg cgcgcccgtc ccccgcgggc gccgcggagc cggggcccg cgcgcgtccg 60
cgctcgaccc gcggacaggt gcgcctgccg ggcgggtgagt tcgcatggg ggacgccttc 120
ggggagggat atccggccga cggcgagaca cccgtgcaca cgggtgcgcct gcggcccttc 180
cacatcgacg agaccgccgt caccaacgcc cggttcgccg ccttcgtcaa ggcgaccggc 240
catgtgaccg acgccgaacg cttcggtctc tcggccgtct tccacctggt cgtegcgcgc 300
ccggacgccg acgtcctcgg cagcgccgcc ggcgccccct ggtggatcaa cgtgcggggc 360
gcccactggc gccgccccga gggcgcccg cccgacatca cggcgccggc gaaccatccg 420
gtcgtccacg tctcctggaa cgatgccacc gcctacgcgc ggtgggcccg caagcgcccg 480
cccaccgagg ccgaatggga gtacgccgcc cgcgggggac tggccggccg ccgctacgcc 540
tggggcgacg agctgacccc gggcgcccg tggcgctgca acatctggca gggcgcttc 600
ccgcacgtca acacggccga ggacgggcac ctgagcaccg caccggtcaa gtcctaccgg 660
cccaacggcc acggcctgtg gaacaccgcg ggcaacgtgt gggaatggtg ctccgactgg 720
ttctcgccca cctactacgc cgaatcacc accgtcgacc cgcacggccc cgggaccggg 780
gcggcacggg tgctgcgcgg cggctcctac ctgtgccacg actcctactg caaccgctac 840
cgggtcgccg cccgctcctc caacaccccg gactcctcgt cgggcaacct cggattccgc 900
tgcgccaacg acgcggacct cacgtccgga tcagccgctg agtga 945

<210> 56
<211> 314
<212> PRT
<213> Streptomyces coelicolor

<400> 56

```

Met Ala Val Ala Ala Pro Ser Pro Ala Ala Ala Ala Glu Pro Gly Pro
1          5          10          15

Ala Ala Arg Pro Arg Ser Thr Arg Gly Gln Val Arg Leu Pro Gly Gly
20          25          30

Glu Phe Ala Met Gly Asp Ala Phe Gly Glu Gly Tyr Pro Ala Asp Gly
35          40          45

Glu Thr Pro Val His Thr Val Arg Leu Arg Pro Phe His Ile Asp Glu
50          55          60

Thr Ala Val Thr Asn Ala Arg Phe Ala Ala Phe Val Lys Ala Thr Gly
65          70          75          80

His Val Thr Asp Ala Glu Arg Phe Gly Ser Ser Ala Val Phe His Leu
85          90          95

Val Val Ala Ala Pro Asp Ala Asp Val Leu Gly Ser Ala Ala Gly Ala
100         105         110

Pro Trp Trp Ile Asn Val Arg Gly Ala His Trp Arg Arg Pro Glu Gly
115         120         125

Ala Arg Ser Asp Ile Thr Gly Arg Pro Asn His Pro Val Val His Val
130         135         140

Ser Trp Asn Asp Ala Thr Ala Tyr Ala Arg Trp Ala Gly Lys Arg Leu
145         150         155         160

Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Leu Ala Gly
165         170         175

Arg Arg Tyr Ala Trp Gly Asp Glu Leu Thr Pro Gly Gly Arg Trp Arg
180         185         190

Cys Asn Ile Trp Gln Gly Arg Phe Pro His Val Asn Thr Ala Glu Asp
195         200         205

Gly His Leu Ser Thr Ala Pro Val Lys Ser Tyr Arg Pro Asn Gly His
210         215         220

Gly Leu Trp Asn Thr Ala Gly Asn Val Trp Glu Trp Cys Ser Asp Trp
225         230         235         240

Phe Ser Pro Thr Tyr Tyr Ala Glu Ser Pro Thr Val Asp Pro His Gly
245         250         255

Pro Gly Thr Gly Ala Ala Arg Val Leu Arg Gly Gly Ser Tyr Leu Cys
260         265         270

His Asp Ser Tyr Cys Asn Arg Tyr Arg Val Ala Ala Arg Ser Ser Asn
275         280         285

Thr Pro Asp Ser Ser Ser Gly Asn Leu Gly Phe Arg Cys Ala Asn Asp
290         295         300

```

Ala Asp Leu Thr Ser Gly Ser Ala Ala Glu
305 310

<210> 57
<211> 1005
<212> DNA
<213> Corynebacterium efficiens

<400> 57
gtggttcgcc atcgactggg ccaccggccc tgcacactga ggattacgtc catgagtaac 60
tgctgctccc cgtcaagcgc acaatggcgt accactaccc gggatttatac agatcctgtc 120
aatccccacca ctccatgcaa cccggaacaa tcccgcgatg ctgtgacact gccgggtgga 180
gctttccaca tgggcgatca tcacggggag gggatcccg cggacgggga ggggccagta 240
catgaggttc acctcgcccc cttcggcatt aatgtcacca cggtcacgaa tgccgagttc 300
ggacgattta ttgaagccac aggggtatacg acgacagcgg aacgctacgg tgtctcggct 360
gtattctacg cagcgttcca agggcaacgc gctgacattc ttcgccagggt tcccggcgtg 420
ccctgggtggc tggcgggtcaa ggggtgcgaac tggcagcgtc ccaacggccc cggatccacc 480
ctggacggggc ttgaggacca ccccgctcgtt cacgtttcct gggatgatgc cgttgccctac 540
tgcacctggg ctggcgggtcg tctgcccacc gaagccgagt gggaatacgc cgcccgggggt 600
ggactgcagg gcgcacgata tgcctggggg gataacctcg ccctagacgg gaggtggaac 660
tgcaatatct ggcagggggg cttcccatg gagaacaccg ccgcgggatgg ttacctcacc 720
actgcaccgg tgaagaccta cacgccaat ggatacggtc tgtggcagat ggcaggggaat 780
gtatgggaat ggtgccagga ctggtttgat gcggagtact actcccgtgc ttcctccatc 840
aaccgcgggg gaccggatac cgggtgcgcgc cgggtgatgc gcggaggctc gtatctctgc 900
catgattcct actgcaacag ataccgggtg gccgcccga attcgaacac cccggattcc 960
acctcgggga ataccggttt cgggtgcgtt ttcgatagtc cttga 1005

<210> 58
<211> 334
<212> PRT
<213> Corynebacterium efficiens

<400> 58

Met Val Arg His Arg Leu Gly His Arg Pro Cys Thr Leu Arg Ile Thr
1 5 10 15

Ser Met Ser Asn Cys Cys Ser Pro Ser Ser Ala Gln Trp Arg Thr Thr
20 25 30

Thr Arg Asp Leu Ser Asp Pro Val Asn Pro Thr Thr Pro Cys Asn Pro
35 40 45

Glu Gln Ser Arg Asp Ala Val Thr Leu Pro Gly Gly Ala Phe His Met
50 55 60

Gly Asp His His Gly Glu Gly Tyr Pro Ala Asp Gly Glu Gly Pro Val
65 70 75 80

His Glu Val His Leu Ala Pro Phe Gly Ile Asn Val Thr Thr Val Thr
85 90 95

Asn Ala Glu Phe Gly Arg Phe Ile Glu Ala Thr Gly Tyr Thr Thr Thr

100	105	110
Ala Glu Arg Tyr Gly Val Ser 115	Ala Val Phe Tyr Ala 120	Ala Phe Gln Gly 125
Gln Arg Ala Asp Ile Leu Arg 130	Gln Val Pro Gly Val 135	Pro Trp Trp Leu 140
Ala Val Lys Gly Ala Asn Trp 145	Gln Arg Pro Asn Gly 150	Pro Gly Ser Thr 155
Leu Asp Gly Leu Glu Asp His 165	Pro Val Val His Val 170	Ser Trp Asp Asp 175
Ala Val Ala Tyr Cys Thr Trp 180	Ala Gly Gly Arg Leu Pro 185	Thr Glu Ala 190
Glu Trp Glu Tyr Ala Ala Arg 195	Gly Gly Leu Gln Gly 200	Ala Arg Tyr Ala 205
Trp Gly Asp Asn Leu Ala Leu 210	Asp Gly Arg Trp Asn 215	Cys Asn Ile Trp 220
Gln Gly Gly Phe Pro Met Glu 225	Asn Thr Ala Ala Asp 230	Gly Tyr Leu Thr 235
Thr Ala Pro Val Lys Thr Tyr 245	Thr Pro Asn Gly Tyr 250	Gly Leu Trp Gln 255
Met Ala Gly Asn Val Trp Glu 260	Trp Cys Gln Asp Trp 265	Phe Asp Ala Glu 270
Tyr Tyr Ser Arg Ala Ser Ser 275	Ile Asn Pro Arg Gly 280	Pro Asp Thr Gly 285
Ala Arg Arg Val Met Arg Gly 290	Gly Gly Ser Tyr Leu 295	Cys His Asp Ser Tyr 300
Cys Asn Arg Tyr Arg Val Ala 305	Ala Arg Asn Ser Asn 310	Thr Pro Asp Ser 315
Thr Ser Gly Asn Thr Gly Phe 325	Arg Cys Val Phe Asp 330	Ser Pro

<210> 59
<211> 1017
<212> DNA
<213> Novosphingobium aromaticivorans

<400> 59	
atggcgcaac cattccgatac gacggcgggc agtcgtacaa gtattgaacg ccatctcgaa	60
cccaattgca ggagcacgta gcgaatggta gaacgccccg gcatgagcct gatcgaaggc	120
ggcactttca ccatggggctc ggaagccttc tacccggagg aagcgccgct tcgccgggtg	180
aaggtagaca gcttctggat cgatgaagcg ccggtgacga acgcacagtt cgccgcattc	240
gtggaggcca cgggatacgt cactgtggcc gagatcgagc cggatcccaa ggactacccc	300
ggcatgctcc cgggcatgga ccgcgcggga tcgctggtgt tccagaaaac agcagggccg	360
gtcgacatgg cggatgcgtc caactggtgg cactttacct ttggcgctg ctggaagcat	420

ccacttggac cgggcagttc catcgatggg atcgaggacc atcccgtcgt tcacgtcgcc 480
tatgccgatg ccgaggccta tgccaaatgg gcgggcaagg atctgccgac cgaagccgag 540
ttcgaatatg ctgcgcgcgg cgggttggac ggttccgaat tttcctgggg agacgaactc 600
gcacctgaag gccggatgat ggccaactac tggcaaggcc tgtttccctt cgccaaccag 660
tgcctcgatg gctgggaacg gacatcgccc gtccgcaact tcccgcccaa cggtatggt 720
ctttacgaca tgatcgggaa cacgtgggag tggacctgcg attggtgggc cgacaagccg 780
ctgactccgc aaaggaatc ggcattgctg cgcatcagca atccgcgcgg cggcaagctc 840
aaggacagct tcgaccgctc gcaaccgca atgcgcatcg gccggaaggt cataaagggc 900
ggttcgcacc tgtgtgcggc caattactgc cagcgctatc gccccgcagc acgccatcct 960
gaaatggttg ataccgcgac gacgcacatc ggcttcaggt gtgtggtgcg gccctga 1017

<210> 60
<211> 338
<212> PRT
<213> Novosphingobium aromaticivorans
<400> 60

Met Ala Gln Pro Phe Arg Ser Thr Ala Ala Ser Arg Thr Ser Ile Glu
1 5 10 15

Arg His Leu Glu Pro Asn Cys Arg Ser Thr Ser Arg Met Val Glu Arg
20 25 30

Pro Gly Met Arg Leu Ile Glu Gly Gly Thr Phe Thr Met Gly Ser Glu
35 40 45

Ala Phe Tyr Pro Glu Glu Ala Pro Leu Arg Arg Val Lys Val Asp Ser
50 55 60

Phe Trp Ile Asp Glu Ala Pro Val Thr Asn Ala Gln Phe Ala Ala Phe
65 70 75 80

Val Glu Ala Thr Gly Tyr Val Thr Val Ala Glu Ile Glu Pro Asp Pro
85 90 95

Lys Asp Tyr Pro Gly Met Leu Pro Gly Met Asp Arg Ala Gly Ser Leu
100 105 110

Val Phe Gln Lys Thr Ala Gly Pro Val Asp Met Ala Asp Ala Ser Asn
115 120 125

Trp Trp His Phe Thr Phe Gly Ala Cys Trp Lys His Pro Leu Gly Pro
130 135 140

Gly Ser Ser Ile Asp Gly Ile Glu Asp His Pro Val Val His Val Ala
145 150 155 160

Tyr Ala Asp Ala Glu Ala Tyr Ala Lys Trp Ala Gly Lys Asp Leu Pro
165 170 175

Thr Glu Ala Glu Phe Glu Tyr Ala Ala Arg Gly Gly Leu Asp Gly Ser
180 185 190

Glu Phe Ser Trp Gly Asp Glu Leu Ala Pro Glu Gly Arg Met Met Ala

195	200	205
Asn Tyr Trp Gln Gly Leu Phe Pro Phe Ala Asn Gln Cys Leu Asp Gly 210 215 220		
Trp Glu Arg Thr Ser Pro Val Arg Asn Phe Pro Pro Asn Gly Tyr Gly 225 230 235		
Leu Tyr Asp Met Ile Gly Asn Thr Trp Glu Trp Thr Cys Asp Trp Trp 245 250 255		
Ala Asp Lys Pro Leu Thr Pro Gln Arg Lys Ser Ala Cys Cys Ala Ile 260 265 270		
Ser Asn Pro Arg Gly Gly Lys Leu Lys Asp Ser Phe Asp Pro Ser Gln 275 280 285		
Pro Ala Met Arg Ile Gly Arg Lys Val Ile Lys Gly Gly Ser His Leu 290 295 300		
Cys Ala Ala Asn Tyr Cys Gln Arg Tyr Arg Pro Ala Ala Arg His Pro 305 310 315 320		
Glu Met Val Asp Thr Ala Thr Thr His Ile Gly Phe Arg Cys Val Val 325 330 335		

Arg Pro

<210> 61
 <211> 1119
 <212> DNA
 <213> Mesorhizobium loti

<400> 61
 atggggccac gaggtcgagg tcaaaaaccg catgaaaggc gacgcggtca tgttcgacat 60
 tgccgggaag ttctagccga tagcgggtgg gcggtgatg gagatgagca cgccgtgtca 120
 ttctgggatc ttctgatgaa cgccctgcc gaagtcttcg agcgcgctgc agccgaacgg 180
 tcgtaccccc gaattggtctg gatccccggc ggtaccttcc tgatgggctc agacaaccac 240
 tatccggagg aggcaccggc ccaccgggtc agggctcgacg gcttctggat ggacaaattc 300
 accgtctcca accgcgactt cgaacgcttc gttgcggcga caggacatgt cactcttgcc 360
 gagaaaccgc ccaatcccgga cgactatccc ggtgccttac ccgatctgct ggctccgtcc 420
 tcgatgatgt tcaggaagcc ggccggccct gtcgaccttg gcaatcacta caattgggtg 480
 gtctatgtcc gcggcgccaa ctggcgccat ccacgcgggc cggaagtac aatcaagaag 540
 gttgcagatc atccggtcgt gcatgtggcc tacgaggatg tcgtggccta tgccaactgg 600
 gcaggcaagg aacttccac cgaggccgag tgggaattcg cggcgcgagg cggcctcgat 660
 gccgccgaat acgtctgggg caacgagctt acgccggccg ggaagcacat ggccaacatc 720
 tggcaaggag actttcccta ccggaatact gtcgacgacg gttacgaata tacggcccca 780
 gtaggtctgt tcccggccaa cgactacggt ctctacgaca tggccggcaa tgtctggcaa 840
 tggacgaccg actggtacca ggaccacaag gcgatcgaca gcccgtgctg caccgctgtc 900
 aatccgcgtg gcggccatcg cgaagcgagc tatgacacc ggctacctga cgttaagatc 960
 cctcgcaagg tcaccaaggg tggctcccat ctgtgcgcgc cgaactactg tcggcgctac 1020

cgccccgccc cgcaatggc gcaacccgtc gacactgcaa tctcccatct cggttttcgc 1080
tgcacgtgc gaaggaaaat ggaattgaac gcgcagtaa 1119

<210> 62
<211> 372
<212> PRT
<213> Mesorhizobium loti

<400> 62

Met Gly Pro Arg Gly Arg Gly Gln Lys Pro His Glu Arg Arg Arg Gly
1 5 10 15

His Val Arg His Cys Arg Glu Val Leu Ala Asp Ser Gly Trp Ala Ala
20 25 30

Asp Gly Asp Glu His Ala Val Ser Phe Arg Asp Leu Ser Met Asn Ala
35 40 45

Pro Ala Glu Val Phe Glu Arg Ala Ala Ala Glu Arg Ser Tyr Pro Gly
50 55 60

Met Val Trp Ile Pro Gly Gly Thr Phe Leu Met Gly Ser Asp Asn His
65 70 75 80

Tyr Pro Glu Glu Ala Pro Ala His Arg Val Arg Val Asp Gly Phe Trp
85 90 95

Met Asp Lys Phe Thr Val Ser Asn Arg Asp Phe Glu Arg Phe Val Ala
100 105 110

Ala Thr Gly His Val Thr Leu Ala Glu Lys Pro Ala Asn Pro Asp Asp
115 120 125

Tyr Pro Gly Ala Leu Pro Asp Leu Leu Ala Pro Ser Ser Met Met Phe
130 135 140

Arg Lys Pro Ala Gly Pro Val Asp Leu Gly Asn His Tyr Asn Trp Trp
145 150 155 160

Val Tyr Val Arg Gly Ala Asn Trp Arg His Pro Arg Gly Pro Ala Ser
165 170 175

Thr Ile Lys Lys Val Ala Asp His Pro Val Val His Val Ala Tyr Glu
180 185 190

Asp Val Val Ala Tyr Ala Asn Trp Ala Gly Lys Glu Leu Pro Thr Glu
195 200 205

Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Asp Ala Ala Glu Tyr
210 215 220

Val Trp Gly Asn Glu Leu Thr Pro Ala Gly Lys His Met Ala Asn Ile
225 230 235 240

Trp Gln Gly Asp Phe Pro Tyr Arg Asn Thr Val Asp Asp Gly Tyr Glu
245 250 255

Tyr Thr Ala Pro Val Gly Ser Phe Pro Ala Asn Asp Tyr Gly Leu Tyr

260

265

270

Asp Met Ala Gly Asn Val Trp Gln Trp Thr Thr Asp Trp Tyr Gln Asp
275 280 285

His Lys Ala Ile Asp Ser Pro Cys Cys Thr Ala Val Asn Pro Arg Gly
290 295 300

Gly His Arg Glu Ala Ser Tyr Asp Thr Arg Leu Pro Asp Val Lys Ile
305 310 315 320

Pro Arg Lys Val Thr Lys Gly Gly Ser His Leu Cys Ala Pro Asn Tyr
325 330 335

Cys Arg Arg Tyr Arg Pro Ala Ala Arg Met Ala Gln Pro Val Asp Thr
340 345 350

Ala Ile Ser His Leu Gly Phe Arg Cys Ile Val Arg Arg Lys Met Glu
355 360 365

Leu Asn Ala Gln
370

<210> 63
<211> 1251
<212> DNA
<213> Burkholderia fungorum

<400> 63
atgaagagtg aaagagatcg agagcccgca aagtcgtccc gctcgaacgg gtcggtcgca 60
gcaacccaaa cgcgcgccgg tcgctgtcgc aaactaatgt tgtggggcgc cctgctcgtc 120
atactgccc cctgtgtcgg cgccgcggtc agttgggcct tcacgccgca cgcacccgct 180
caccgcgaaa tcgttttcgg cgacggcacg catgggtccgc tcggcatggc gtgggtgccc 240
ggcggccagt tcctcatggg cagcgacgcc aaacaggcgc aaccgaacga acgccccgcg 300
cacaagggtca aggtgcacgg cttctggatg gaccgccatc acgtgaccaa cgccgaattc 360
cgccgcttcg tcgaagcgac cggctacgtc accacggccg agaagaaacc cgactgggag 420
accctgaaag tccagttgcc gcccggcacg ccgcgcccgc ccgagagcgc gatgggtggcg 480
ggtgcaatgg tgctcgtcgg caccagccgt cccgtgccgc tagacgacta ttcgcagtgg 540
tggcgctatg tgccgtggcg taactggcgt catccagccg ggcctgagag caacatcatc 600
ggtaaagatg atcaccccggt ggttcaagtg tcctacgaag atgcgcaggc ttatgcgaaa 660
tgggcccggca agcgtctgcc gaccgaagcc gaatgggaat tcgccgcgcg cggcggcctc 720
gaacaggcca cgtatgcgtg gggcgatcag ttctctccca acggcaaaca gatggccaac 780
gtctggcagg gccagcagcc gcagtctttc cccgttgtca acccgaaagc ggggtggcgcg 840
ctcgtgtaca gtccggtggg tactttcccg gccaacggct acggcctttc cgacatgacc 900
ggcaacgcct ggagtgggg tgccgactgg tatcgcgcg atcagttcag gcgtgaggcg 960
gtaagcacca gcgcgatcga caatccggtg ggcccagcgc agtcgtggga ccccgagac 1020
cagggcggtgc ccgtcaacgc gcccaagcgt gtcacacgcg gcggttcggt cctctgcaac 1080
gaaatctatt gcctgagcta cgggcccagc gcgagacgcg gcaccgatcc ctacaacagc 1140
atgtcgcata tgggcttcgg gctgggtgat gacgaagaca cctggaaaga agccggtgct 1200
cgccaggctt cggcgaaagc tgccggcgcg cctggaaccc ctggcggtta g 1251

<210> 64
 <211> 416
 <212> PRT
 <213> Burkholderia fungorum

<400> 64

Met Lys Ser Glu Arg Asp Arg Glu Pro Ala Lys Ser Ser Arg Ser Asn
 1 5 10 15

Gly Ser Val Ala Ala Thr Gln Thr Arg Ala Gly Arg Val Arg Lys Leu
 20 25 30

Met Leu Trp Gly Ala Leu Leu Val Ile Leu Pro Ala Cys Val Gly Ala
 35 40 45

Ala Val Ser Trp Ala Phe Thr Pro His Ala Pro Ala His Pro Gln Ile
 50 55 60

Val Phe Gly Asp Gly Thr His Gly Pro Leu Gly Met Ala Trp Val Pro
 65 70 75 80

Gly Gly Gln Phe Leu Met Gly Ser Asp Ala Lys Gln Ala Gln Pro Asn
 85 90 95

Glu Arg Pro Ala His Lys Val Lys Val His Gly Phe Trp Met Asp Arg
 100 105 110

His His Val Thr Asn Ala Glu Phe Arg Arg Phe Val Glu Ala Thr Gly
 115 120 125

Tyr Val Thr Thr Ala Glu Lys Lys Pro Asp Trp Glu Thr Leu Lys Val
 130 135 140

Gln Leu Pro Pro Gly Thr Pro Arg Pro Pro Glu Ser Ala Met Val Ala
 145 150 155 160

Gly Ala Met Val Phe Val Gly Thr Ser Arg Pro Val Pro Leu Asp Asp
 165 170 175

Tyr Ser Gln Trp Trp Arg Tyr Val Pro Gly Ala Asn Trp Arg His Pro
 180 185 190

Ala Gly Pro Glu Ser Asn Ile Ile Gly Lys Asp Asp His Pro Val Val
 195 200 205

Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp Ala Gly Lys
 210 215 220

Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu
 225 230 235 240

Glu Gln Ala Thr Tyr Ala Trp Gly Asp Gln Phe Ser Pro Asn Gly Lys
 245 250 255

Gln Met Ala Asn Val Trp Gln Gly Gln Gln Pro Gln Ser Phe Pro Val
 260 265 270

Val Asn Pro Lys Ala Gly Gly Ala Leu Gly Thr Ser Pro Val Gly Thr

275		280		285
Phe	Pro	Ala	Asn	Gly
290				295
	Tyr	Gly	Leu	Ser
			Asp	Met
				300
	Thr	Gly	Asn	Ala
				Trp
Gln	Trp	Val	Ala	Asp
305				310
	Tyr	Arg	Ala	Asp
				315
	Phe	Arg	Arg	Glu
				320
Val	Ser	Thr	Ser	Ala
				325
	Ile	Asp	Asn	Pro
				330
	Val	Gly	Pro	Ser
				335
Asp	Pro	Ala	Asp	Gln
				340
	Gly	Val	Pro	Val
				345
	Asn	Ala	Pro	Lys
				350
Arg	Gly	Gly	Ser	Phe
				355
	Leu	Cys	Asn	Glu
				360
	Ile	Tyr	Cys	Leu
				365
Pro	Ser	Ala	Arg	Arg
				370
	Gly	Thr	Asp	Pro
				375
	Tyr	Asn	Ser	Met
				380
	Ser	His	Leu	
Gly	Phe	Arg	Leu	Val
385				390
	Met	Asp	Glu	Asp
				395
	Thr	Trp	Lys	Glu
				400
Arg	Gln	Ala	Ser	Ala
				405
	Lys	Ala	Ala	Gly
				410
	Ala	Pro	Gly	Thr
				415

<210> 65
 <211> 912
 <212> DNA
 <213> Sinorhizobium meliloti

<400> 65	
atggtctggtg	60
ttccccggagc	
gaccttcacg	
atgggggtcga	
acgaccatta	
cccggaggaa	60
gcgcccgtgc	
atccggtaac	
cgctcgacga	
ttctggatcg	
atgtgacacc	
ggtaacgaac	120
cgccagtttc	
tcgaattcgt	
aaatgcgacg	
gggcatgtga	
ccttcgcgga	
aagaaagccg	180
cgcgccgaag	
actatccggg	
cgctccgcca	
tccaatctaa	
gggcccgggtc	
gctcgtcttc	240
acacccccga	
agcgaccgct	
gcagggaacg	
gatatatcgc	
agtgggtgat	
attcacgctg	300
ggtgccaaact	
ggcgggcacc	
gctcggggcg	
aagagcagca	
tcggagcgat	
tctggatcat	360
ccggtcgtcc	
atgtcgctta	
cagcgacgca	
aaggcctatg	
ccgaatgggc	
cggcaaggac	420
ctccccgaccg	
agaccgagtg	
ggagctggcg	
gcccgcggcg	
gcctcgatgg	
ggctgaattt	480
tcctggggcg	
gcgagcttgc	
gccgggcgga	
aatcacatgg	
ccaatacttg	
gcagggaagt	540
tttccggctg	
agaattctat	
ggacgatggt	
ttcgcgcgaa	
catcgccggt	
cagatatttac	600
ccgcccgaacg	
gctacggcct	
ctacgacatg	
atcggaatg	
tgtgggagtg	
gaccacggat	660
tactggtccg	
tgcgccaccc	
ggaagcggcc	
gccaaagcctt	
gctgcattcc	
gagcaatccc	720
cgcaatgccg	
atgccgatgc	
gagtatcgat	
ccggcgggcg	
gcgtgaaagt	
tccgcgcccgg	780
gtgctcaagg	
gtggatcgca	
tctctgcgcg	
ccgaactact	
gccggcggtg	
ccgccctgcg	840
gcgaggcacg	
cccaggaaat	
cgacacgacg	
accagccatg	
tcggtttccg	
atgtgtcagg	900
cgcggttcgat	
aa	912

<210> 66
 <211> 303
 <212> PRT
 <213> Sinorhizobium meliloti

<400> 66

Met	Val	Trp	Val	Pro	Gly	Ala	Thr	Phe	Met	Met	Gly	Ser	Asn	Asp	His
1				5				10					15		
Tyr	Pro	Glu	Glu	Ala	Pro	Val	His	Pro	Val	Thr	Val	Asp	Gly	Phe	Trp
		20						25					30		
Ile	Asp	Val	Thr	Pro	Val	Thr	Asn	Arg	Gln	Phe	Leu	Glu	Phe	Val	Asn
	35						40					45			
Ala	Thr	Gly	His	Val	Thr	Phe	Ala	Glu	Arg	Lys	Pro	Arg	Ala	Glu	Asp
	50					55					60				
Tyr	Pro	Gly	Ala	Pro	Pro	Ser	Asn	Leu	Arg	Ala	Gly	Ser	Leu	Val	Phe
65				70						75					80
Thr	Pro	Pro	Lys	Arg	Pro	Leu	Gln	Gly	Thr	Asp	Ile	Ser	Gln	Trp	Trp
			85						90					95	
Ile	Phe	Thr	Leu	Gly	Ala	Asn	Trp	Arg	His	Pro	Leu	Gly	Arg	Lys	Ser
			100					105					110		
Ser	Ile	Gly	Ala	Ile	Leu	Asp	His	Pro	Val	Val	His	Val	Ala	Tyr	Ser
		115					120					125			
Asp	Ala	Lys	Ala	Tyr	Ala	Glu	Trp	Ala	Gly	Lys	Asp	Leu	Pro	Thr	Glu
	130					135					140				
Thr	Glu	Trp	Glu	Leu	Ala	Ala	Arg	Gly	Gly	Leu	Asp	Gly	Ala	Glu	Phe
145					150					155					160
Ser	Trp	Gly	Gly	Glu	Leu	Ala	Pro	Gly	Gly	Asn	His	Met	Ala	Asn	Thr
				165					170					175	
Trp	Gln	Gly	Ser	Phe	Pro	Val	Glu	Asn	Ser	Met	Asp	Asp	Gly	Phe	Ala
			180					185					190		
Arg	Thr	Ser	Pro	Val	Arg	Phe	Tyr	Pro	Pro	Asn	Gly	Tyr	Gly	Leu	Tyr
		195					200					205			
Asp	Met	Ile	Gly	Asn	Val	Trp	Glu	Trp	Thr	Thr	Asp	Tyr	Trp	Ser	Val
	210					215					220				
Arg	His	Pro	Glu	Ala	Ala	Ala	Lys	Pro	Cys	Cys	Ile	Pro	Ser	Asn	Pro
225					230					235					240
Arg	Asn	Ala	Asp	Ala	Asp	Ala	Ser	Ile	Asp	Pro	Ala	Ala	Ser	Val	Lys
				245					250					255	
Val	Pro	Arg	Arg	Val	Leu	Lys	Gly	Gly	Ser	His	Leu	Cys	Ala	Pro	Asn
			260					265					270		
Tyr	Cys	Arg	Arg	Tyr	Arg	Pro	Ala	Ala	Arg	His	Ala	Gln	Glu	Ile	Asp
		275					280					285			
Thr	Thr	Thr	Ser	His	Val	Gly	Phe	Arg	Cys	Val	Arg	Arg	Val	Arg	
		290				295					300				

<210> 67
<211> 1065
<212> DNA
<213> *Microscilla* sp.

<400> 67
atgaaataca tttttttagt tcttttctta tgggccttga cccgatgtac cggaaagtat 60
gaggacaaga gagtggaaac tgatacttcc agaccaaaag ccgaagcgtc agatataaaa 120
gttcccgaag gaatggctta tattcccgcg ggccagtaca tgatgggagg taaatcagac 180
caggcttata aggatgaata tccccgccat aacgtgaagg tttcggcttt ttatatggac 240
cttacagaag tgaccaatgc ggagtttaag cggtttgtag acgaaacggg ctacgtgacc 300
attgctgaga aagatattga ctgggaagag ttaaagtctc aggtgccaca gggtagccccg 360
aagcctcctg attctgtgct tcaggcaggt tcaactgggtt tcaagcagac agatgaaccc 420
gtttctctcc aggattattc acagtgggtg gaatggacta tcggagccaa ctggcgaaat 480
ccggagggtc caggtagtac gattgaggat cgtatggatc atccgggtgt acacgtttcc 540
tttgaagatg tccaagcgtg tgccgattgg gccggtaagc gcctgcctac tgaggcagaa 600
tggaatggg ccgccatggg aggccaaaat gacgtgaaat atccatgggg aatgaatcg 660
gtcgaacaag catccgataa agcaaaacttt tggcagggga attttcaca tcaaaactat 720
gccctcgatg gattcgaacg caccgcccct gtacgtcctc tcccagcgaa tgggtacggc 780
ctatatgata tggctggcaa tgtgtgggaa tgggtgccagg ataagtatga tgtcaatgct 840
tatgaaagct ataagcaaaa aggactgaca gaagaccca cgggttctga gcactacaac 900
gacctagggg aaccgtatac tcctaagcat gtgatcagag ggggttcttt cctatgcaat 960
gacagctact gtagtgggta tcgtgtttca cgtcgtatga gttccagtag agattcaggt 1020
tttaatcata cgggattcag gtgtgtgaaa gatgtaaatg gatag 1065

<210> 68
<211> 354
<212> PRT
<213> *Microscilla* sp.

<400> 68
Met Lys Tyr Ile Phe Leu Val Leu Phe Leu Trp Ala Leu Thr Arg Cys
1 5 10 15
Thr Gly Lys Tyr Glu Asp Lys Arg Val Glu Thr Asp Thr Ser Arg Pro
20 25 30
Lys Ala Glu Ala Ser Asp Ile Lys Val Pro Glu Gly Met Ala Tyr Ile
35 40 45
Pro Ala Gly Gln Tyr Met Met Gly Gly Lys Ser Asp Gln Ala Tyr Lys
50 55 60
Asp Glu Tyr Pro Arg His Asn Val Lys Val Ser Ala Phe Tyr Met Asp
65 70 75 80
Leu Thr Glu Val Thr Asn Ala Glu Phe Lys Arg Phe Val Asp Glu Thr
85 90 95
Gly Tyr Val Thr Ile Ala Glu Lys Asp Ile Asp Trp Glu Glu Leu Lys
100 105 110

Ser Gln Val Pro Gln Gly Thr Pro Lys Pro Pro Asp Ser Val Leu Gln
115 120 125

Ala Gly Ser Leu Val Phe Lys Gln Thr Asp Glu Pro Val Ser Leu Gln
130 135 140

Asp Tyr Ser Gln Trp Trp Glu Trp Thr Ile Gly Ala Asn Trp Arg Asn
145 150 155 160

Pro Glu Gly Pro Gly Ser Thr Ile Glu Asp Arg Met Asp His Pro Val
165 170 175

Val His Val Ser Phe Glu Asp Val Gln Ala Tyr Ala Asp Trp Ala Gly
180 185 190

Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Trp Ala Ala Met Gly Gly
195 200 205

Gln Asn Asp Val Lys Tyr Pro Trp Gly Asn Glu Ser Val Glu Gln Ala
210 215 220

Ser Asp Lys Ala Asn Phe Trp Gln Gly Asn Phe Pro His Gln Asn Tyr
225 230 235 240

Ala Leu Asp Gly Phe Glu Arg Thr Ala Pro Val Arg Ser Phe Pro Ala
245 250 255

Asn Gly Tyr Gly Leu Tyr Asp Met Ala Gly Asn Val Trp Glu Trp Cys
260 265 270

Gln Asp Lys Tyr Asp Val Asn Ala Tyr Glu Ser Tyr Lys Gln Lys Gly
275 280 285

Leu Thr Glu Asp Pro Thr Gly Ser Glu His Tyr Asn Asp Pro Arg Glu
290 295 300

Pro Tyr Thr Pro Lys His Val Ile Arg Gly Gly Ser Phe Leu Cys Asn
305 310 315 320

Asp Ser Tyr Cys Ser Gly Tyr Arg Val Ser Arg Arg Met Ser Ser Ser
325 330 335

Arg Asp Ser Gly Phe Asn His Thr Gly Phe Arg Cys Val Lys Asp Val
340 345 350

Asn Gly

<210> 69
<211> 876
<212> DNA
<213> Pseudomonas putida KT2440

<400> 69
atgggtgcacg tgccggggcgg cgagttcagc tttggttcaa gccgctttta cgacgaagaa 60
ggccccgcctc accccgccaa ggtgtccggc ttctggattg acgtgcatcc ggtcaccaac 120
gccagttcg cgcgcttcgt caaggccacg gggatatgtca cccatgccga gcgcggtacc 180
cgtgtcgagg acgacctgc cctgcccgcac gcgctgcgga taccgggtgc gatggtgttt 240

catcaggggtg cggacgtgct cggccccggc tggcagttcg tgcccggcgc caactggcga 300
caccgcgaag ggccgggcag cagcctggcc gggctggaca accatccggt ggtgcagatc 360
gccctggaag atgccaggc ctatgccgc tgggcaggcc gcgaactgcc cagcgaggcg 420
cagctggaat acgccatgcg cggcggcctg accgatgccg acttcagctg ggggtaccacc 480
gagcagccca agggcaagct catggccaat acctggcagg gtcagttccc ttatcgcaat 540
gcggcgaagg atggttttac cgggtacatcg cccgtgggtt gcttcccggc caacggcttt 600
ggcctgttcg atgccggcgg caatgtcttg gagctgactc gcacgggcta tcggccaggc 660
catgacgcac agcgcgacgc caagctcgac ccctcaggcc cggccctgag tgacagcttc 720
gacccggcag accccggcgt gccggtggcg gtaatcaaag gcggctcgca cctgtgttcg 780
gcggaccgct gcatgcgcta ccgccctcg gcacgccagc cgcagccggt gttcatgacg 840
acctgcacg tgggtttcag aacgattcgg caatga 876

<210> 70
<211> 291
<212> PRT
<213> Pseudomonas putida KT2440

<400> 70

Met Val His Val Pro Gly Gly Glu Phe Ser Phe Gly Ser Ser Arg Phe
1 5 10 15

Tyr Asp Glu Glu Gly Pro Pro His Pro Ala Lys Val Ser Gly Phe Trp
20 25 30

Ile Asp Val His Pro Val Thr Asn Ala Gln Phe Ala Arg Phe Val Lys
35 40 45

Ala Thr Gly Tyr Val Thr His Ala Glu Arg Gly Thr Arg Val Glu Asp
50 55 60

Asp Pro Ala Leu Pro Asp Ala Leu Arg Ile Pro Gly Ala Met Val Phe
65 70 75 80

His Gln Gly Ala Asp Val Leu Gly Pro Gly Trp Gln Phe Val Pro Gly
85 90 95

Ala Asn Trp Arg His Pro Gln Gly Pro Gly Ser Ser Leu Ala Gly Leu
100 105 110

Asp Asn His Pro Val Val Gln Ile Ala Leu Glu Asp Ala Gln Ala Tyr
115 120 125

Ala Arg Trp Ala Gly Arg Glu Leu Pro Ser Glu Ala Gln Leu Glu Tyr
130 135 140

Ala Met Arg Gly Gly Leu Thr Asp Ala Asp Phe Ser Trp Gly Thr Thr
145 150 155 160

Glu Gln Pro Lys Gly Lys Leu Met Ala Asn Thr Trp Gln Gly Gln Phe
165 170 175

Pro Tyr Arg Asn Ala Ala Lys Asp Gly Phe Thr Gly Thr Ser Pro Val
180 185 190

Gly Cys Phe Pro Ala Asn Gly Phe Gly Leu Phe Asp Ala Gly Gly Asn
195 200 205

Val Trp Glu Leu Thr Arg Thr Gly Tyr Arg Pro Gly His Asp Ala Gln
210 215 220

Arg Asp Ala Lys Leu Asp Pro Ser Gly Pro Ala Leu Ser Asp Ser Phe
225 230 235 240

Asp Pro Ala Asp Pro Gly Val Pro Val Ala Val Ile Lys Gly Gly Ser
245 250 255

His Leu Cys Ser Ala Asp Arg Cys Met Arg Tyr Arg Pro Ser Ala Arg
260 265 270

Gln Pro Gln Pro Val Phe Met Thr Thr Ser His Val Gly Phe Arg Thr
275 280 285

Ile Arg Gln
290

<210> 71
<211> 780
<212> DNA
<213> Ralstonia metallidurans

<400> 71
atgggtcgcg gcgggatggt gttcgtcggc accaacagcc cgggtgccgct gcgcgaatac 60
tggcgctggt ggcgtttcgt acctggcgcg gactggcgtc acccgaccgg cccggggcagt 120
tccatcgaag gcaaggacaa tcatcccgtc gtgcaggtct cgtatgaaga cgcgcaggcg 180
tacgccaagt gggccggcaa gcgtctgccc accgaggccg agtgggagtt tgccgcccgt 240
ggcggcctgg agcaggccac ctacgcctgg ggtgacaagt tcgcgccgga tggccggcag 300
atggcgaatg tctggcaggg ccagcaggtg cagccgttcc cgggtggtcag cgccaaggcg 360
ggcggcgcgg ctggcaccag tgctgtcggc acgttcccgg gcaatggcta tgggctctat 420
gacatgaccg gcaacgcctg gcagtgggtg gccgactggt atcgcgcgga ccagttccgc 480
cgcgaagcca cggtgggcgg agtgctgcag aatccgaccg gccgggccga ttcgtgggac 540
ccgaccgaac ctggcgtgcc ggtgtcggcg cccaagcggg tcacgcgcgg tggctcgttc 600
ctctgcaacg aggacttctg cctcagctac cgcccagtg cccggcgcgg taccgaccgg 660
tacaccagca tgtcgcacct aggcttccgg ctcgtgatgg atgacgcccg ttgggcagaa 720
gttcgcaagc agccagccgt ggcaatggcc gcgggcgggc agcagaacgt gcagaaataa 780

<210> 72
<211> 259
<212> PRT
<213> Ralstonia metallidurans

<400> 72

Met Val Ala Gly Gly Met Val Phe Val Gly Thr Asn Ser Pro Val Pro
1 5 10 15

Leu Arg Glu Tyr Trp Arg Trp Trp Arg Phe Val Pro Gly Ala Asp Trp
20 25 30

Arg His Pro Thr Gly Pro Gly Ser Ser Ile Glu Gly Lys Asp Asn His

35	40	45
Pro Val Val Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp		
50	55	60
Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg		
65	70	75 80
Gly Gly Leu Glu Gln Ala Thr Tyr Ala Trp Gly Asp Lys Phe Ala Pro		
	85	90 95
Asp Gly Arg Gln Met Ala Asn Val Trp Gln Gly Gln Gln Val Gln Pro		
	100	105 110
Phe Pro Val Val Ser Ala Lys Ala Gly Gly Ala Ala Gly Thr Ser Ala		
	115	120 125
Val Gly Thr Phe Pro Gly Asn Gly Tyr Gly Leu Tyr Asp Met Thr Gly		
	130	135 140
Asn Ala Trp Gln Trp Val Ala Asp Trp Tyr Arg Ala Asp Gln Phe Arg		
	145	150 155 160
Arg Glu Ala Thr Val Ala Ala Val Leu Gln Asn Pro Thr Gly Pro Ala		
	165	170 175
Asp Ser Trp Asp Pro Thr Glu Pro Gly Val Pro Val Ser Ala Pro Lys		
	180	185 190
Arg Val Thr Arg Gly Gly Ser Phe Leu Cys Asn Glu Asp Phe Cys Leu		
	195	200 205
Ser Tyr Arg Pro Ser Ala Arg Arg Gly Thr Asp Pro Tyr Thr Ser Met		
	210	215 220
Ser His Leu Gly Phe Arg Leu Val Met Asp Asp Ala Arg Trp Ala Glu		
	225	230 235 240
Val Arg Lys Gln Pro Ala Val Ala Met Ala Ala Gly Gly Gln Gln Asn		
	245	250 255

Val Gln Lys

<210> 73
 <211> 876
 <212> DNA
 <213> Prochlorococcus marinus

<400> 73	
gtgaccacat ctttgccagt agagatggta accatccccg cagggctcta tcgagttggc	60
tgtgatcgct gctatccgga tggttcagtt cgctgctatc cggaggaaac acccgcgca	120
gaagtgcagc ttgactcatt ccagatcgac gtagggccag tcaccaatgc ccagttccga	180
gctttcggtta gcgccacgca gcatctcaca gtctcggagc taccacctga tccaacgctc	240
tatcccgatc tagcgcccga ggaacgcac cctgaatcag ttgtctttca accgcctcca	300
gcaacggtgg atcgagcaa acccttgagc tgggtggacc tcatggctgg ggctgattgg	360
cgtcaccccc aaggaccga aagcacgac gatggccttg atgatcacc tgctgtgcat	420

gtcgccatg cgcagccat cgcctatgcc cattgggctg gcaagcgtct cccctctgct 480
 gaagagtggg aagtagccgc cgcggggggt cttgtcgatg cccaatacgc ctgggggaat 540
 gaactcactc ccaataaccg ctggatggcg aacatctggc aaggtccttt cccttggcac 600
 aacgaggagc tagacggctg gttctggacc tcgcccgttg gcagctttcc tgccaacggc 660
 tatggactct tggatgtttg cggcaatgtg tgggaatgga ccaactctgt ttatcccggtg 720
 gcgtcaggcc accaggaacg gcgaactatc aaaggcggat cgtttctctg cgcagataat 780
 tactgcgtac gttatcgacc ctctgcacta caaggccaga cagtagacac tgccacctgt 840
 cacatgggct ttcgctgtgc aaaaggaggg ccttga 876

<210> 74
 <211> 291
 <212> PRT
 <213> *Prochlorococcus marinus*

<400> 74

Met Thr Thr Ser Leu Pro Val Glu Met Val Thr Ile Pro Ala Gly Leu
 1 5 10 15

Tyr Arg Val Gly Cys Asp Arg Cys Tyr Pro Asp Gly Ser Val Arg Cys
 20 25 30

Tyr Pro Glu Glu Thr Pro Ala Arg Glu Val Gln Leu Asp Ser Phe Gln
 35 40 45

Ile Asp Val Gly Pro Val Thr Asn Ala Gln Phe Arg Ala Phe Val Ser
 50 55 60

Ala Thr Gln His Leu Thr Val Ser Glu Leu Pro Pro Asp Pro Thr Leu
 65 70 75 80

Tyr Pro Asp Leu Ala Pro Glu Glu Arg Ile Pro Glu Ser Val Val Phe
 85 90 95

Gln Pro Pro Pro Ala Thr Val Asp Arg Ser Lys Pro Leu Ser Trp Trp
 100 105 110

Thr Leu Met Ala Gly Ala Asp Trp Arg His Pro Gln Gly Pro Glu Ser
 115 120 125

Thr Ile Asp Gly Leu Asp Asp His Pro Val Val His Val Ala Tyr Ala
 130 135 140

Asp Ala Ile Ala Tyr Ala His Trp Ala Gly Lys Arg Leu Pro Ser Ala
 145 150 155 160

Glu Glu Trp Glu Val Ala Ala Arg Gly Gly Leu Val Asp Ala Gln Tyr
 165 170 175

Ala Trp Gly Asn Glu Leu Thr Pro Asn Asn Arg Trp Met Ala Asn Ile
 180 185 190

Trp Gln Gly Pro Phe Pro Trp His Asn Glu Glu Leu Asp Gly Trp Phe
 195 200 205

Trp Thr Ser Pro Val Gly Ser Phe Pro Ala Asn Gly Tyr Gly Leu Leu

210 215 220

Asp Val Cys Gly Asn Val Trp Glu Trp Thr Asn Ser Val Tyr Pro Val
225 230 235 240

Ala Ser Gly His Gln Glu Arg Arg Thr Ile Lys Gly Gly Ser Phe Leu
245 250 255

Cys Ala Asp Asn Tyr Cys Val Arg Tyr Arg Pro Ser Ala Leu Gln Gly
260 265 270

Gln Thr Val Asp Thr Ala Thr Cys His Met Gly Phe Arg Cys Ala Lys
275 280 285

Gly Gly Pro
290

<210> 75
<211> 1017
<212> DNA
<213> *Caulobacter crescentus* CB15

<400> 75
ttgggaaaac tgacggcgct tcccgtcctg atgcttctgg cgctggccgg ctgcgggccag 60
ccggcgccca aggcttgcc tggcgacctg ccggttccag atccccagaa ccgcacggcg 120
ggtatggttc ggctggcggg cggcgacttc cagatgggcy ctgcgccgct gcgtccggag 180
gagggaccgc cccagacggt caccgtcccg ccgttctgga tcgatcagac agaggtcacc 240
aacgcgcct tcgcgcggtt cgtcgaggcc acgggttatc gcaccgtggc cgagcgaccg 300
ctcgaccccc cgcgctacgc ccacgtaccg gcggcgcagc ggcgccggc ctcgctcgtc 360
ttcgtggggg cgaagggggc gaggtcggac gacccctccc aatgggtggc ggtgatcccc 420
ggcgccgact ggcgccatcc cgaaggtccc ggctcgaaca tccggggcag ggacgcctgg 480
ccggtggtgc atatcgcggt ggaggacgcc atggcctacg cccgctggct gggccgtgac 540
ctgcccacag aggcgcaatg ggagtacgcc gcgcgcggcg ggctggttgg caagcgctac 600
acctggggcg accaggetca ggatcctgca aagccgcgcg ccaatacttg gcaaggcgtg 660
ttccccggcc aggaccttgg caatgacggc ttcaaggcca agcccgcgcc ggtcgggtgc 720
ttccccgcca acggctatgg cctgcgcgac atggccggca atgtctggga gtggacccgc 780
gactggttca agccgggccc ggatccggtc agcgtcctcg aaaccggcgg gccgcccag 840
gcccgcgcg tggatcccca ggacccgaac acgcccgaag acgtcgtgaa gggcggttcg 900
ttcctgtgcy ccgacgacta ctgcttccgc tatcgacctg cggcgcggaac gccggggccg 960
ccggacagcy gcgcacgca tgcggtttc cgcaccgtgc tccgcgccga gcgctga 1017

<210> 76
<211> 338
<212> PRT
<213> *Caulobacter crescentus* CB15

<400> 76
Met Gly Lys Leu Thr Ala Leu Pro Val Leu Met Leu Leu Ala Leu Ala
1 5 10 15

Gly Cys Gly Gln Pro Ala Pro Lys Ala Cys Leu Ala Asp Leu Pro Val
20 25 30

Pro Asp Pro Gln Asn Arg Thr Ala Gly Met Val Arg Leu Ala Gly Gly
35 40 45

•Asp Phe Gln Met Gly Ala Ala Pro Leu Arg Pro Glu Glu Gly Pro Pro
50 55 60

Gln Thr Val Thr Val Pro Pro Phe Trp Ile Asp Gln Thr Glu Val Thr
65 70 75 80

Asn Ala Ala Phe Ala Arg Phe Val Glu Ala Thr Gly Tyr Arg Thr Val
85 90 95

Ala Glu Arg Pro Leu Asp Pro Ala Arg Tyr Ala His Val Pro Ala Ala
100 105 110

Gln Arg Arg Pro Ala Ser Leu Val Phe Val Gly Ala Lys Gly Ala Arg
115 120 125

Ser Asp Asp Pro Ser Gln Trp Trp Gln Val Ile Pro Gly Ala Asp Trp
130 135 140

Arg His Pro Glu Gly Pro Gly Ser Asn Ile Arg Gly Arg Asp Ala Trp
145 150 155 160

Pro Val Val His Ile Ala Trp Glu Asp Ala Met Ala Tyr Ala Arg Trp
165 170 175

Leu Gly Arg Asp Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg
180 185 190

Gly Gly Leu Val Gly Lys Arg Tyr Thr Trp Gly Asp Gln Ala Gln Asp
195 200 205

Pro Ala Lys Pro Arg Ala Asn Thr Trp Gln Gly Val Phe Pro Ala Gln
210 215 220

Asp Leu Gly Asn Asp Gly Phe Lys Ala Lys Pro Ala Pro Val Gly Cys
225 230 235 240

Phe Pro Pro Asn Gly Tyr Gly Leu Arg Asp Met Ala Gly Asn Val Trp
245 250 255

Glu Trp Thr Arg Asp Trp Phe Lys Pro Gly Leu Asp Pro Val Ser Val
260 265 270

Leu Glu Thr Gly Gly Pro Pro Glu Ala Arg Ala Leu Asp Pro Glu Asp
275 280 285

Pro Asn Thr Pro Lys His Val Val Lys Gly Gly Ser Phe Leu Cys Ala
290 295 300

Asp Asp Tyr Cys Phe Arg Tyr Arg Pro Ala Ala Arg Thr Pro Gly Pro
305 310 315 320

Pro Asp Ser Gly Ala Ser His Val Gly Phe Arg Thr Val Leu Arg Ala
325 330 335

Glu Arg

<210> 77
 <211> 900
 <212> DNA
 <213> Mycobacterium tuberculosis H37Rv

<400> 77
 gtgctgaccg agttggttga cctgcccggc ggatcggtcc gcatgggctc gacgcgcttc 60
 taccgccgaag aagcgccgat tcataccgtg accgtgcgcg cctttgcggt agagcgacac 120
 ccggtgacca acgcgcaatt tgccgaattc gtctccgcga caggctatgt gacggttgca 180
 gaacaacccc ttgaccccg gctctaccca ggagtggacg cagcagacct gtgtcccggt 240
 gcgatggtgt tttgtccgac ggccggggccg gtcgacctgc gtgactggcg gcaatggtgg 300
 gactgggtac ctggcgccctg ctggcgccat ccgtttggcc gggacagcga tatcgccgac 360
 cgagccggcc acccggtcgt acaggtggcc tatccggacg ccgtggccta cgcacgatgg 420
 gctggtcgac gcctaccgac cgaggccgag tgggagtacg cggcccgtgg cggaaccacg 480
 gcaacctatg cgtggggcga ccaggagaag cgggggggca tgctcatggc gaacacctgg 540
 cagggcggtt ttccttaccg caacgacggt gcattgggct ggggtgggaac ctccccggtg 600
 ggcaggtttc cggccaacgg gtttggttg ctcgacatga tcggaaacgt ttgggagtgg 660
 accaccaccg agttctatcc acaccatcgc atcgatccac cctcgacggc ctgctgcgca 720
 ccggtcaagc tcgctacagc cgccgacccg acgatcagcc agaccctcaa gggcggctcg 780
 cacctgtgcg cgccggagta ctgccaccgc taccgcccg cggcgcgctc gccgcagtcg 840
 caggacaccg cgaccaccca tatcggttcc cgggtgcgtgg ccgaccgggt gtccgggtag 900

<210> 78
 <211> 299
 <212> PRT
 <213> Mycobacterium tuberculosis H37Rv

<400> 78
 Met Leu Thr Glu Leu Val Asp Leu Pro Gly Gly Ser Phe Arg Met Gly
 1 5 10 15
 Ser Thr Arg Phe Tyr Pro Glu Glu Ala Pro Ile His Thr Val Thr Val
 20 25 30
 Arg Ala Phe Ala Val Glu Arg His Pro Val Thr Asn Ala Gln Phe Ala
 35 40 45
 Glu Phe Val Ser Ala Thr Gly Tyr Val Thr Val Ala Glu Gln Pro Leu
 50 55 60
 Asp Pro Gly Leu Tyr Pro Gly Val Asp Ala Ala Asp Leu Cys Pro Gly
 65 70 75 80
 Ala Met Val Phe Cys Pro Thr Ala Gly Pro Val Asp Leu Arg Asp Trp
 85 90 95
 Arg Gln Trp Trp Asp Trp Val Pro Gly Ala Cys Trp Arg His Pro Phe
 100 105 110
 Gly Arg Asp Ser Asp Ile Ala Asp Arg Ala Gly His Pro Val Val Gln
 115 120 125

Val Ala Tyr Pro Asp Ala Val Ala Tyr Ala Arg Trp Ala Gly Arg Arg
130 135 140

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Thr Thr
145 150 155 160

Ala Thr Tyr Ala Trp Gly Asp Gln Glu Lys Pro Gly Gly Met Leu Met
165 170 175

Ala Asn Thr Trp Gln Gly Arg Phe Pro Tyr Arg Asn Asp Gly Ala Leu
180 185 190

Gly Trp Val Gly Thr Ser Pro Val Gly Arg Phe Pro Ala Asn Gly Phe
195 200 205

Gly Leu Leu Asp Met Ile Gly Asn Val Trp Glu Trp Thr Thr Thr Glu
210 215 220

Phe Tyr Pro His His Arg Ile Asp Pro Pro Ser Thr Ala Cys Cys Ala
225 230 235 240

Pro Val Lys Leu Ala Thr Ala Ala Asp Pro Thr Ile Ser Gln Thr Leu
245 250 255

Lys Gly Gly Ser His Leu Cys Ala Pro Glu Tyr Cys His Arg Tyr Arg
260 265 270

Pro Ala Ala Arg Ser Pro Gln Ser Gln Asp Thr Ala Thr Thr His Ile
275 280 285

Gly Phe Arg Cys Val Ala Asp Pro Val Ser Gly
290 295

<210> 79

<211> 7

<212> PRT

<213> Artificial

<220>

<223> conserved domain in prokaryotes and prokaryotes

<220>

<221> DOMAIN

<222> (1)..(7)

<223> conserved domain

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Gly or Ala

<400> 79

Arg Val Xaa Xaa Gly Xaa Ser

1

5

<210> 80
<211> 630
<212> DNA
<213> *Oncorhynchus mykiss*

```
<400> 80
tcagggtggct gctgccccct ggtggttgcc tgtcagagga gcagactgga ggcaccctga      60
gggccccgac tccagcatca cagacaggct ggaccaccct gtgctgcatg tgtcatggca      120
ggacgctgtg gcctactgct cctgggccta caagagacta cccacagagg ctgagtggga      180
gtacgcctgc agagggggcc tacaggagag actttaccctg tgggggaaca aactgaaacc      240
taaaggacag cactacgcca acctctggca gggaaagtcc cccacacaca actcagaaga      300
ggacgggtac actaaaacct caccagttaa gtcatttcct gcaaattggc atggcctgta      360
caacatggta gggaatgcat gggagtggac atctgactgg tggactgtac accacaccac      420
agatgaacag cacaaccctg caggtccacc atcaggcaca gaccgagtga agaaaggagg      480
ctcctacatg tgccataagt catactgtta caggtacagg tgtgcagcac ggagtcagaa      540
caccctgac agctctgcct ctaacctagg gttccgctgt gtctcccagg agcagccgta      600
acctttcacc ctgaccctg acatgggtag                                     630
```

<210> 81
<211> 655
<212> DNA
<213> *Danio rerio*

<220>
<221> misc_feature
<222> (590)..(590)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (626)..(626)
<223> n is a, c, g, or t

```
<400> 81
caaatgggtt tatttacata aaaaaatcct cttagtgtga agtgtaagac agtgagatta      60
gtgatgtttg aggttatgga tcaacatcag aggcgcagcg gaagcccaag ttcgaggctg      120
aactgtccgg tgtgttctga ctgcgagcgg cacacctgta tctgtagcag taagacttgt      180
ggcacatgta ggatcctcct ttcttgactc tgtctgtccc tgattctggt ccctttgggt      240
taaacttgtc ttctgcagtg tgatgcacag tccaccagtc tgccgtccac tcccacgcat      300
ttcccaccat gtcatacagg ccaaagccat tgggaggaaa agacatcacc ggggatgtgt      360
tggcatagcc gtcctctgca gtgttgtgat tagggaaatc tccctgccac aggttagcat      420
agtgtgtccc tcttggcatt aatttatctc cccatgggta catcctgtcc tgtagtcctc      480
ctctacaggc caactcccat tcagcttctg taggaagtct gcgtttggcc cattgacagt      540
acgcccgtgc atcatcccat gaaacatgca gagcaggggtg attcattctn gtgtgtatgg      600
ttgaatctgg tcctttctgg tgtctncagt ctgcaccttt cactggtgac cacca          655
```

<210> 82
<211> 773
<212> DNA
<213> *Oryzias latipes*

<220>

<221> misc_feature
<222> (690)..(690)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (755)..(755)
<223> n is a, c, g, or t

<400> 82
tctcctttttt tccataaata acattagagt ccttacattc tgcctttaca tacattgtca 60
gagacagtac aaaaaatctg cctttgtaaa attagagtta caaaaatata ttttagattt 120
gactttcttca gaattgtcgg tggcagcaaa agaatcggat tgatctcatg acaagagcgt 180
gagccagaag ttcttggatc aaactgattt gggttctgtca tcgtttctgt tcagcagcac 240
agcgaaaacc aagattggaa gcggagctgt ctggagtgtt ttggcttcga gcagcacatc 300
tgtacctgta acaataagac ttgtggcaca tgtacgagcc tcctttcttc accttatctg 360
tgcctgacgg aggaccctgt gggttgtgct gatggtctgt tgtgtggtgc acgctccacc 420
agtctgaggt ccaactcccat gcgttcccca ccatgtcata cagacaaaaa gcattgcctg 480
ggaaggacat caccggggag gttttagtgt agccatcctc tgcagagttg tgtgctggga 540
attccccctg ccagagggtg gcgtaatgct gtcccttttg gtttagcttg tttccccagg 600
ggtagagtct gtccttcagg ccgccctgc aggcaacctc ccaactctgcc tcagtgggaa 660
gtctcttggt gacccaggag cagtaagccn aggcattcatt cccagaaacc tgaacgacgg 720
atgatccatc ctgtctgtga tgttgaggtc tggancttca gggtgcttcc agt 773

<210> 83
<211> 566
<212> DNA
<213> Xenopus laevis

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (47)..(47)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (81)..(81)
<223> n is a, c, g, or t

<400> 83
atatgnaact aaaggtaatg taattggaat gatggatttc acaaggnetg agagttccct 60
attgtctctg cttgtcgtgt nacaggtcac ggagccggcg ccacacagcg aaatcccagg 120
ttggaggccg agctgtcggg tgtattctga cttcgagcag cacagcgata cctgtagcaa 180
taggactcat ggcacatgta ggagcctcct ttcttcactc tatcatttcc cgtagaaggt 240
cctttcgggt tgtgaacctc atctgctgta tgatgagtgt cccaccaatc agatgtccac 300
tccaagcat tccccacat gttatataga ccataaccat tggctgggaa agcagttaca 360
ggtgaagtct gcacataacc atcctctcca gtgttttggg ttggaaaatc cccctgccag 420
acattcgcat aatgttgtec ctttggttcc agcttggtcc cccatggaaa aatcctgttc 480
tcaagtcctc cgcggcaggc gtattccac tcagcttcag ttggaaggcg tttacctgcc 540
caggtgcaga aagcagaagc atcatt 566

<210> 84
<211> 647
<212> DNA
<213> *Silurana tropicalis*

<400> 84
gccgcttttt tttttttttt tttttttttt catcacaaaa ataattttat taataaaata 60
ggattttgtg ttcattctta ttatgaagga caaggaatgt cattgaaatt tttgttttca 120
caaggtcttg ggagttcctt cctgctcagg tcattttgca gtggtcacgg agccgacgcc 180
acgcagcggga atcccagggt agaggccgag ctgtcagggtg tattctgact tcgagcagca 240
cagcgatacc tgtagcagta ggactcatgg cacatgtatg agcctccttt tttcaccttg 300
tcttttcccg taaaaggacc tttcgggttg taagtctcat ctgctgtatg atgagtgtcc 360
caccaatcgg atgtccactc ccaagcattt cccaccatgt tatataggct ataaccattg 420
gctgggaaag cggttacagg tgaagtctgc acatagccgt cctctccagt gttttgggtt 480
ggaaattccc cctgccagac attcgcataa tgttctccct ttggttccag cttgttcccc 540
cacggaaaaa gctgttctc aagtcccca cgggaggcat attccactc agcttctgtc 600
ggaaggcgct taccgcacca ggtgcagaag gcagaagcat cgttcca 647

<210> 85
<211> 636
<212> DNA
<213> *Salmo salar*

<400> 85
atagacattt tttaaatatt ttacaacaaa atatattcca taaatatcca catgtcatgc 60
ggtaatcctg catttcatga agaacactga catcactggc tgtatgaaga ggtgcacttg 120
atttgtttcg cctggcgggc aagataggca gagttagcac cctagactag agccaatggc 180
gaatggtaca aaaagggaaa agtcagacta cccatgtcag ggtcaagggt aaaaggttac 240
ggctgctcct gggagacaca gcggaaccct aggttagagg cagagctgtc aggggtgttc 300
tgactccgtg ctgcacacct gtacctgtaa cagtatgact tatggcacat gtaggagcct 360
cctttcttca ctcggtctgt gcctgatggg ggacctgccg ggttgtgccg ttcactctgtg 420
gtgtgggtgta cagtccacca gtcagatgtc cactcccatg cattccctac catgttgtac 480
aggccatagc catttgcagg aaatgacttc actggtgagg ttttgggtgta cccgtcctct 540
tctgagttgt gtgtggggaa ctttccctgc cagagggttg cgtagtgtg tcctttaggt 600
ttcagtttgt tccccacgg gtaaagtctg tcctgt 636

<210> 86
<211> 415
<212> DNA
<213> *Sus scrofa*

<400> 86
agtttctctg gaccaacacc ggagaggatg gcttccgagg aactgcccct gttgatgcct 60
ttcctcccaa tgggttatggc ctttacaata tagtagggaa cgctgggaa tggacctcag 120
actggtggac cattcaccat gctgctgaag aaacaattaa cccatcaagt tcttctgtct 180
gcaccgaata acagagccgc cactacgtga tgaaagcaga gaaaggcccc cttctctggga 240
aagaccgggt gaagaaaggg ggatectata tgtgccataa gtcctactgc tacaggtagc 300
gctgtgctgc tcgaagccag aacacgccgg acagctcggc ttcaaactct gggttccgct 360

gtgcagctga ccaccagccc accacaggct gagtcaggaa gagtcttccc gaatc 415

<210> 87
<211> 595
<212> DNA
<213> Bos taurus

<400> 87
ccacgcgtcc gggggcaaca aactgcagcc gaaaggccag cattatagcc aacatcttgg 60
caaggcgagt ttctgtgac caacaccggg gaggacggct tccgaggac cgcgctgtt 120
gacgccttcc ctccaatgg ttattggctt atacaatata gtagggaacg cctgggagtg 180
gacttcagac tgggtggactg ttcaccattc tgctgaagaa acgattaacc caaaaggccc 240
cccttctggg aaagaccggg tgaagaaagg tggatcctac atgtgccata aatcctattg 300
ctacaggatc cgctgtgctg ctcgaagcca gaacacaccg gacagctctg cttcgaatct 360
gggattccgt tgtgcagctg accacctgcc caccacaggc taagagccaa aaagagcctt 420
cccgaaccgg agaagtcgtg tctactctgc acgcggtctc cctcagaagg ctgaacaacc 480
tgctgtgaag aattcccacc ccaaggtggg ttacatacct tgcccagtgg ccaaaggacc 540
tatggcaaga ccaaattgct gagctgatca gcattgtgctg tttattgggg gatgg 595

<210> 88
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1608)
<223> hSULF3

<400> 88
atg cta ctg ctg tgg gtg tgc gca gcc ttg gcg ctg gcg gta 48
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val
1 5 10 15
ctg gcc ccc gga gca ggg gag cag agg cgg aga gca gcc aaa gcg ccc 96
Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro
20 25 30
aat gtg gtg ctg gtc gtg agc gac tcc ttc gat gga agg tta aca ttt 144
Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe
35 40 45
cat cca gga agt cag gta gtg aaa ctt cct ttt atc aac ttt atg aag 192
His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys
50 55 60
aca cgt ggg act tcc ttt ctg aat gcc tac aca aac tct cca att tgt 240
Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys
65 70 75 80
tgc cca tca cgc gca gca atg tgg agt ggc ctc ttc act cac tta aca 288
Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr
85 90 95
gaa tct tgg aat aat ttt aag ggt cta gat cca aat tat aca aca tgg 336
Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp
100 105 110
atg gat gtc atg gag agg cat ggc tac cga aca cag aaa ttt ggg aaa 384
Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys
115 120 125
ctg gac tat act tca gga cat cac tcc att agt aat cgt gtg gaa gcg 432
Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala
130 135 140

tgg Trp 145	aca Thr	aga Arg	gat Asp	gtt Val	gct Ala 150	ttc Phe	tta Leu	ctc Leu	aga Arg	caa Gln 155	gaa Glu	ggc Gly	agg Arg	ccc Pro	atg Met 160	480
gtt Val	aat Asn	ctt Leu	atc Ile	cgt Arg 165	aac Asn	agg Arg	act Thr	aaa Lys	gtc Val 170	aga Arg	gtg Val	atg Met	gaa Glu	agg Arg	gat Asp 175	528
tgg Trp	cag Gln	aat Asn	aca Thr 180	gac Asp	aaa Lys	gca Ala	gta Val	aac Asn 185	tgg Trp	tta Leu	aga Arg	aag Lys	gaa Glu 190	gca Ala	att Ile	576
aat Asn	tac Tyr	act Thr 195	gaa Glu	cca Pro	ttt Phe	gtt Val	att Ile 200	tac Tyr	ttg Leu	gga Gly	tta Leu	aat Asn 205	tta Leu	cca Pro	cac His	624
cct Pro	tac Tyr 210	cct Pro	tca Ser	cca Pro	tct Ser 215	tct Ser	gga Gly	gaa Glu	aat Asn	ttt Phe 220	gga Gly	tct Ser	tca Ser	aca Thr	ttt Phe	672
cac His 225	aca Thr	tct Ser	ctt Leu	tat Tyr	tgg Trp 230	ctt Leu	gaa Glu	aaa Lys	gtg Val	tct Ser 235	cat His	gat Asp	gcc Ala	atc Ile	aaa Lys 240	720
atc Ile	cca Pro	aag Lys	tgg Trp 245	tca Ser	cct Pro	ttg Leu	tca Ser	gaa Glu	atg Met 250	cac His	cct Pro	gta Val	gat Asp	tat Tyr 255	tac Tyr	768
tct Ser	tct Ser	tat Tyr 260	aca Thr	aaa Lys	aac Asn	tgc Cys	act Thr	gga Gly 265	aga Arg	ttt Phe	aca Thr	aaa Lys 270	aaa Glu	gaa Glu	att Ile	816
aag Lys	aat Asn	att Ile 275	aga Arg	gca Ala	ttt Phe	tat Tyr	tat Tyr 280	gct Ala	atg Met	tgt Cys	gct Ala	gag Glu	aca Thr	gat Asp	gcc Ala	864
atg Met 290	ctt Leu	ggt Gly	gaa Glu	att Ile	att Ile	ttg Leu 295	gcc Ala	ctt Leu	cat His	caa Gln	tta Leu	gat Asp	ctt Leu	ctt Leu	cag Gln	912
aaa Lys 305	act Thr	att Ile	gtc Val	ata Ile	tac Tyr 310	tcc Ser	tca Ser	gac Asp	cat His	gga Gly 315	gag Glu	ctg Leu	gcc Ala	atg Met	gaa Glu 320	960
cat His	cga Arg	cag Gln	ttt Phe 325	tat Tyr	aaa Lys	atg Met	agc Ser	atg Met	tac Tyr 330	gag Glu	gct Ala	agt Ser	gca Ala	cat His 335	gtt Val	1008
ccg Pro	ctt Leu	ttg Leu	atg Met 340	atg Met	gga Gly	cca Pro	gga Gly	att Ile 345	aaa Lys	gcc Ala	ggc Gly	cta Leu	caa Gln	gta Val	tca Ser	1056
aat Asn	gtg Val	gtt Val 355	tct Ser	ctt Leu	gtg Val	gat Asp	att Ile 360	tac Tyr	cct Pro	acc Thr	atg Met	ctt Leu	gat Asp	att Ile	gct Ala	1104
gga Gly	att Ile 370	cct Pro	ctg Leu	cct Pro	cag Gln	aac Asn 375	ctg Leu	agt Ser	gga Gly	tac Tyr	tct Ser	ttg Leu	ttg Leu	ccg Pro	tta Leu	1152
tca Ser 385	tca Ser	gaa Glu	aca Thr	ttt Phe 390	aag Lys	aat Asn	gaa Glu	cat His	aaa Lys	gtc Val 395	aaa Lys	aac Asn	ctg Leu	cat His	cca Pro 400	1200
ccc Pro	tgg Trp	att Ile	ctg Leu	agt Ser 405	gaa Glu	ttc Phe	cat His	gga Gly	tgt Cys 410	aat Asn	gtg Val	aat Asn	gcc Ala	tcc Ser	acc Thr	1248
tac Tyr	atg Met	ctt Leu	cga Arg 420	act Thr	aac Asn	cac His	tgg Trp	aaa Lys 425	tat Tyr	ata Ile	gcc Ala	tat Tyr	tcg Ser	gat Asp	ggg Gly	1296
gca Ala	tca Ser	ata Ile 435	ttg Leu	cct Pro	caa Gln	ctc Leu	ttt Phe 440	gat Asp	ctt Leu	tcc Ser	tcg Ser	gat Pro	cca Pro	gat Asp	gaa Glu	1344
tta Leu	aca Thr	aat Asn	gtt Val	gct Ala	gta Val	aaa Lys	ttt Phe	cca Pro	gaa Glu	att Ile	act Thr	tat Tyr	tct Ser	ttg Leu	gat Asp	1392

450	455	460	
cag aag ctt cat tcc att ata aac tac cct aaa gtt tct gct tct gtc Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val 465 470 475 480			1440
cac cag tat aat aaa gag cag ttt atc aag tgg aaa caa agt ata gga His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly 485 490 495			1488
cag aat tat tca aac gtt ata gca aat ctt agg tgg cac caa gac tgg Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp 500 505 510			1536
cag aag gaa cca agg aag tat gaa aat gca att gat cag tgg ctt aaa Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys 515 520 525			1584
acc cat atg aat cca aga gca gtt tga Thr His Met Asn Pro Arg Ala Val 530 535			1611
<p><210> 89 <211> 536 <212> PRT <213> Homo sapiens</p>			
<p><400> 89</p>			
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val 1 5 10 15			
Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro 20 25 30			
Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe 35 40 45			
His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys 50 55 60			
Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys 65 70 75 80			
Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr 85 90 95			
Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp 100 105 110			
Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys 115 120 125			
Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala 130 135 140			
Trp Thr Arg Asp Val Ala Phe Leu Leu Arg Gln Glu Gly Arg Pro Met 145 150 155 160			
Val Asn Leu Ile Arg Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp 165 170 175			
Trp Gln Asn Thr Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile 180 185 190			

Asn Tyr Thr Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His
195 200 205

Pro Tyr Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe
210 215 220

His Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
225 230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr Tyr
245 250 255

Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys Glu Ile
260 265 270

Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu Thr Asp Ala
275 280 285

Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu Asp Leu Leu Gln
290 295 300

Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly Glu Leu Ala Met Glu
305 310 315 320

His Arg Gln Phe Tyr Lys Met Ser Met Tyr Glu Ala Ser Ala His Val
325 330 335

Pro Leu Leu Met Met Gly Pro Gly Ile Lys Ala Gly Leu Gln Val Ser
340 345 350

Asn Val Val Ser Leu Val Asp Ile Tyr Pro Thr Met Leu Asp Ile Ala
355 360 365

Gly Ile Pro Leu Pro Gln Asn Leu Ser Gly Tyr Ser Leu Leu Pro Leu
370 375 380

Ser Ser Glu Thr Phe Lys Asn Glu His Lys Val Lys Asn Leu His Pro
385 390 395 400

Pro Trp Ile Leu Ser Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr
405 410 415

Tyr Met Leu Arg Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly
420 425 430

Ala Ser Ile Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu
435 440 445

Leu Thr Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp
450 455 460

Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val
465 470 475 480

His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly
485 490 495

Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp
500 505 510

Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys
515 520 525

Thr His Met Asn Pro Arg Ala Val
530 535

<210> 90
<211> 1722
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1719)
<223> hSULF4

<400> 90
atg ggg gcg ctg gca gga ttc tgg atc ctc tgc ctc ctc act tat ggt 48
Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly
1 5 10 15
tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta 96
Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu
20 25 30
cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc 144
Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser
35 40 45
cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat 192
Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
50 55 60
gtg ggt tac cac gga tct gag att aaa aca cct act ctt gac aag ctc 240
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu
65 70 75 80
gct gcc gaa gga gtt aaa ctg gag aac tac tat gtc cag cct att tgc 288
Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys
85 90 95
aca cca tcc agg agt cag ttt att act gga aag tat cag ata cac acc 336
Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr
100 105 110
gga ctt caa cat tct atc ata aga cct acc caa ccc aac tgt tta cct 384
Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro
115 120 125
ctg gac aat gcc acc cta cct cag aaa ctg aag gag gtt gga tat tca 432
Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser
130 135 140
acg cat atg gtc gga aaa tgg cac ttg ggt ttt tac aga aaa gaa tgc 480
Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys
145 150 155 160
atg ccc acc aga aga gga ttt gat acc ttt ttt ggt tcc ctt ttg gga 528
Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly
165 170 175
agt ggg gat tac tat aca cac tac aaa tgt gac agt cct ggg atg tgt 576
Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys
180 185 190
ggc tat gac ttg tat gaa aac gac aat gct gcc tgg gac tat gac aat 624
Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn
195 200 205
ggc ata tac tcc aca cag atg tac act cag aga gta cag caa atc tta 672
Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu
210 215 220

gct tcc cat aac ccc aca aag cct ata ttt tta tat att gcc tat caa Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln 225 230 235 240	720
gct gtt cat tca cca ctg caa gct cct ggc agg tat ttc gaa cac tac Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr 245 250 255	768
cga tcc att atc aac ata aac agg agg aga tat gct gcc atg ctt tcc Arg Ser Ile Ile Asn Ile Asn Arg Arg Tyr Ala Ala Met Leu Ser 260 265 270	816
tgc tta gat gaa gca atc aac aac gtg aca ttg gct cta aag act tat Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr 275 280 285	864
ggg ttc tat aac aac agc att atc att tac tct tca gat aat ggt ggc Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly 290 295 300	912
cag cct acg gca gga ggg agt aac tgg cct ctc aga ggt agc aaa gga Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly 305 310 315 320	960
aca tat tgg gaa gga ggg atc cgg gct gta ggc ttt gtg cat agc cca Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro 325 330 335	1008
ctt ctg aaa aac aag gga aca gtg tgt aag gaa ctt gtg cac atc act Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr 340 345 350	1056
gac tgg tac ccc act ctc att tca ctg gct gaa gga cag att gat gag Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu 355 360 365	1104
gac att caa cta gat ggc tat gat atc tgg gag acc ata agt gag ggt Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly 370 375 380	1152
ctt cgc tca ccc cga gta gat att ttg cat aac att gac ccc ata tac Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr 385 390 395 400	1200
acc aag gca aaa aat ggc tcc tgg gca gca ggc tat ggg atc tgg aac Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn 405 410 415	1248
act gca atc cag tca gcc atc aga gtg cag cac tgg aaa ttg ctt aca Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr 420 425 430	1296
gga aat cct ggc tac agc gac tgg gtc ccc cct cag tct ttc agc aac Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn 435 440 445	1344
ctg gga ccg aac cgg tgg cac aat gaa cgg atc acc ttg tca act ggc Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly 450 455 460	1392
aaa agt gta tgg ctt ttc aac atc aca gcc gac cca tat gag agg gtg Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val 465 470 475 480	1440
gac cta tct aac agg tat cca gga atc gtg aag aag ctc cta cgg agg Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg 485 490 495	1488
ctc tca cag ttc aac aaa act gca gtg ccg gtc agg tat ccc ccc aaa Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys 500 505 510	1536
gac ccc aga agt aac cct agg ctc aat gga ggg gtc tgg gga cca tgg Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp 515 520 525	1584
tat aaa gag gaa acc aag aaa aag aag cca agc aaa aat cag gct gag Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu	1632

530	535	540	
aaa aag caa aag aaa agc aaa aaa aag aag aag aaa cag cag aaa gca			1680
Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala			
545	550	555	560
gtc tca ggt tca act tgc cat tca ggt gtt act tgt gga taa			1722
Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly			
	565	570	
<210>	91		
<211>	573		
<212>	PRT		
<213>	Homo sapiens		
<400>	91		
Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly			
1	5	10	15
Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu			
	20	25	30
Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser			
	35	40	45
Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp			
	50	55	60
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu			
65	70	75	80
Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys			
	85	90	95
Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr			
	100	105	110
Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro			
	115	120	125
Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser			
	130	135	140
Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys			
145	150	155	160
Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly			
	165	170	175
Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys			
	180	185	190
Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn			
	195	200	205
Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu			
	210	215	220
Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln			
225	230	235	240

Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr
245 250 255

Arg Ser Ile Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser
260 265 270

Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr
275 280 285

Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
290 295 300

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly
305 310 315 320

Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro
325 330 335

Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr
340 345 350

Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu
355 360 365

Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly
370 375 380

Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr
385 390 395 400

Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn
405 410 415

Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr
420 425 430

Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn
435 440 445

Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly
450 455 460

Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val
465 470 475 480

Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg
485 490 495

Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys
500 505 510

Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp
515 520 525

Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu
530 535 540

Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala
545 550 555 560

Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly
565 570

<210> 92
<211> 1710
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1707)
<223> hSULF5

<400> 92
atg cac acc ctc act ggc ttc tcc ctg gtc agc ctg ctc agc ttc ggc 48
Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly
1 5 10 15
tac ctg tcc tgg gac tgg gcc aag ccg agc ttc gtg gcc gac ggg ccc 96
Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro
20 25 30
ggg gag gct ggc gag cag ccc tcg gcc gct ccg ccc cag cct ccc cac 144
Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His
35 40 45
atc atc ttc atc ctc acg gac gac caa ggc tac cac gac gtg ggc tac 192
Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr
50 55 60
cat ggt tca gat atc gag acc cct acg ctg gac agg ctg gcg gcc aag 240
His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys
65 70 75 80
ggg gtc aag ttg gag aat tat tac atc cag ccc atc tgc acg cct tcg 288
Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser
85 90 95
cgg agc cag ctc ctc act ggc agg tac cag atc cac aca gga ctc cag 336
Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln
100 105 110
cat tcc atc atc cgc cca cag cag ccc aac tgc ctg ccc ctg gac cag 384
His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln
115 120 125
gtg aca ctg cca cag aag ctg cag gag gca ggt tat tcc acc cat atg 432
Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met
130 135 140
gtg ggc aag tgg cac ctg ggc ttc tac cgg aag gag tgt ctg ccc acc 480
Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr
145 150 155 160
cgt cgg ggc ttc gac acc ttc ctg ggc tcg ctc acg ggc aat gtg gac 528
Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp
165 170 175
tat tac acc tat gac aac tgt gat ggc cca ggc gtg tgc ggc ttc gac 576
Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp
180 185 190
ctg cac gag ggt gag aat gtg gcc tgg ggg ctc agc ggc cag tac tcc 624
Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser
195 200 205
act atg ctt tac gcc cag cgc gcc agc cat atc ctg gcc agc cac agc 672
Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser
210 215 220
cct cag cgt ccc ctc ttc ctc tat gtg gcc ttc cag gca gta cac aca 720
Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr
225 230 235 240

ccc Pro	ctg Leu	cag Gln	tcc Ser	cct Pro 245	cgt Arg	gag Glu	tac Tyr	ctg Leu	tac Tyr 250	cgc Arg	tac Tyr	cgc Arg	acc Thr	atg Met 255	ggc Gly	768
aat Asn	gtg Val	gcc Ala	cgg Arg 260	cgg Arg	aag Lys	tac Tyr	gcg Ala	gcc Ala 265	atg Met	gtg Val	acc Thr	tgc Cys	atg Met 270	gat Asp	gag Glu	816
gct Ala	gtg Val	cgc Arg 275	aac Asn	atc Ile	acc Thr	tgg Trp	gcc Ala 280	ctc Leu	aag Lys	cgc Arg	tac Tyr	ggg Gly 285	ttc Phe	tac Tyr	aac Asn	864
aac Asn 290	agt Ser	gtc Val	atc Ile	atc Ile	ttc Phe	tcc Ser 295	agt Ser	gac Asp	aat Asn	ggg Gly 300	ggc Gly	cag Gln	act Thr	ttc Phe	tcg Ser	912
ggg Gly 305	ggc Gly	agc Ser	aac Asn	tgg Trp	ccg Pro 310	ctc Leu	cga Arg	gga Gly	cgc Arg 315	aag Lys	ggc Gly	act Thr	tat Tyr	tgg Trp 320	gaa Glu	960
ggg Gly	ggc Gly	gtg Val	cgg Arg 325	ggc Gly	cta Leu	ggc Gly	ttt Phe	gtc Val	cac His 330	agt Ser	ccc Pro	ctg Leu	ctc Leu	aag Lys 335	cga Arg	1008
aag Lys	caa Gln	cgg Arg	aca Thr 340	agc Ser	cgg Arg	gca Ala	ctg Leu	atg Met 345	cac His	atc Ile	act Thr	gac Asp	tgg Trp 350	tac Tyr	ccg Pro	1056
acc Thr	ctg Leu	gtg Val 355	ggg Gly	ctg Leu	gca Ala	ggg Gly	ggg Gly 360	acc Thr	acc Thr	tca Ser	gca Ala	gcc Ala 365	gat Asp	ggg Gly	cta Leu	1104
gat Asp	ggc Gly	tac Tyr	gac Asp	gtg Val	tgg Trp	ccg Pro 375	gcc Ala	atc Ile	agc Ser	gag Glu	ggc Gly 380	cgg Arg	gcc Ala	tca Ser	cca Pro	1152
cgc Arg 385	acg Thr	gag Glu	atc Ile	ctg Leu	cac His 390	aac Asn	att Ile	gac Asp	cca Pro	ctc Leu 395	tac Tyr	aac Asn	cat His	gcc Ala 400	cag Gln	1200
cat His	ggc Gly	tcc Ser	ctg Leu 405	gag Glu	ggc Gly	ggc Gly	ttt Phe	ggc Gly 410	atc Ile	tgg Trp	aac Asn	acc Thr	gcc Ala 415	gtg Val	cag Gln	1248
gct Ala	gcc Ala	atc Ile	cgc Arg 420	gtg Val	ggg Gly	gag Glu	tgg Trp	aag Lys 425	ctg Leu	ctg Leu	aca Thr	gga Gly	gac Asp 430	ccc Pro	ggc Gly	1296
tat Tyr	ggc Gly	gat Asp 435	tgg Trp	atc Ile	cca Pro	ccg Pro	cag Gln 440	aca Thr	ctg Leu	gcc Ala	acc Thr	ttc Phe 445	ccg Pro	ggg Gly	agc Ser	1344
tgg Trp 450	tgg Trp	aac Asn	ctg Leu	gaa Glu	cga Arg	atg Met 455	gcc Ala	agt Ser	gtc Val	cgc Arg	cag Gln 460	gcc Ala	gtg Val	tgg Trp	ctc Leu	1392
ttc Phe 465	aac Asn	atc Ile	agt Ser	gct Ala	gac Asp 470	cct Pro	tat Tyr	gaa Glu	cgg Arg	gag Glu 475	gac Asp	ctg Leu	gct Ala	ggc Gly	cag Gln 480	1440
cgg Arg	cct Pro	gat Asp	gtg Val 485	gtc Val	cgc Arg	acc Thr	ctg Leu	ctg Leu	gct Ala 490	cgc Arg	ctg Leu	gcc Ala	gaa Glu 495	tat Tyr	aac Asn	1488
cgc Arg	aca Thr	gcc Ala	atc Ile 500	ccg Pro	gta Val	cgc Arg	tac Tyr	cca Pro 505	gct Ala	gag Glu	aac Asn	ccc Pro	cgg Arg 510	gct Ala	cat His	1536
cct Pro	gac Asp	ttt Phe 515	aat Asn	ggg Gly	ggg Gly	gct Ala	tgg Trp 520	ggg Gly	ccc Pro	tgg Trp	gcc Ala	agt Ser 525	gat Asp	gag Glu	gaa Glu	1584
gag Glu 530	gag Glu	gaa Glu	gag Glu	gaa Gly	ggg Gly 535	agg Ala	gct Ala	cga Arg	agc Ser	ttc Phe	tcc Ser 540	cgg Arg	ggg Gly	cgt Arg	cgc Arg	1632
aag Lys	aaa Lys	aaa Lys	tgc Cys	aag Lys	att Ile	tgc Cys	aag Lys	ctt Leu	cga Arg	tcc Ser	ttt Phe	ttc Phe	cgt Arg	aaa Lys	ctc Leu	1680

Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu
260 265 270

Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn
275 280 285

Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser
290 295 300

Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu
305 310 315 320

Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg
325 330 335

Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro
340 345 350

Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu
355 360 365

Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro
370 375 380

Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln
385 390 395 400

His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln
405 410 415

Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly
420 425 430

Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser
435 440 445

Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu
450 455 460

Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln
465 470 475 480

Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn
485 490 495

Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His
500 505 510

Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu
515 520 525

Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg
530 535 540

Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu
545 550 555 560

Asn Thr Arg Leu Met Ser Gln Arg Ile
565

<210> 94
 <211> 2067
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2064)
 <223> hSULF6

<400> 94
 atg cta att tca gga aga gaa gag aac caa ata gac ata tcc aag acc 48
 Met Leu Ile Ser Gly Arg Glu Glu Asn Gln Ile Asp Ile Ser Lys Thr
 1 5 10 15
 aca gag gta gat tgt ttt gtg gtt gaa tta gga agt cta cac aat cct 96
 Thr Glu Val Asp Cys Phe Val Val Glu Leu Gly Ser Leu His Asn Pro
 20 25 30
 aca cgg aac cca cag cga att ttc acc aag cac gtg gcc acc aag tca 144
 Thr Arg Asn Pro Gln Arg Ile Phe Thr Lys His Val Ala Thr Lys Ser
 35 40 45
 tcc agc tcc aaa tgt cag ctg gac caa ggt gga aaa agc ctg gtc cag 192
 Ser Ser Ser Lys Cys Gln Leu Asp Gln Gly Gly Lys Ser Leu Val Gln
 50 55 60
 tgc att tta ccc aga tct tca aag ctc ctc tca ccc ttg tgt ctc ccc 240
 Cys Ile Leu Pro Arg Ser Ser Lys Leu Leu Ser Pro Leu Cys Leu Pro
 65 70 75 80
 cat ccg tgt gga gct tta ctt ctg tat aga tcc tca gga atc gcc tct 288
 His Pro Cys Gly Ala Leu Leu Leu Tyr Arg Ser Ser Gly Ile Ala Ser
 85 90 95
 gct ctt gct gcc ttt aca gac tcc ctc tct agg agc tgc tgg ctg tca 336
 Ala Leu Ala Ala Phe Thr Asp Ser Leu Ser Arg Ser Cys Trp Leu Ser
 100 105 110
 gtg tcc ctg tgc tgt ttg ttt tgc ggt gtt gat ggc aca ttt atg aca 384
 Val Ser Leu Cys Cys Leu Phe Cys Gly Val Asp Gly Thr Phe Met Thr
 115 120 125
 aga aac gcc aga ccc aac att gtc ctg ctg atg gca gat gac ctt gga 432
 Arg Asn Ala Arg Pro Asn Ile Val Leu Leu Met Ala Asp Asp Leu Gly
 130 135 140
 gtg ggg gat ttg tgc tgc tac ggt aat aac tca gtg agc aca cct aat 480
 Val Gly Asp Leu Cys Cys Tyr Gly Asn Asn Ser Val Ser Thr Pro Asn
 145 150 155 160
 att gac cgc ctg gca agt gaa gga gtg agg ctt acc cag cat ctc gca 528
 Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala
 165 170 175
 gct gct tcc atg tgc acc cca agt cgg gct gcc ttc ctg acc ggc cgg 576
 Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg
 180 185 190
 tac ccc atc aga tca ggg atg gtg tct gcc tac aac ctg aac cgt gcc 624
 Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala
 195 200 205
 ttc acg tgg ctt ggt ggg tca ggt ggt ctt ccc acc aat gaa acg act 672
 Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr
 210 215 220
 ttt gcc aag ctg ctg cag cac cgt ggc tac cgc acg gga ctc ata ggc 720
 Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly
 225 230 235 240
 aaa tgg cac ctg ggt ttg agc tgc gcc tct cgg aat gat cac tgt tac 768
 Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr
 245 250 255

cac His	ccg Pro	ctc Leu	aac Asn 260	cat His	ggg Gly	ttt Phe	cac His 265	tac Tyr 265	ttt Phe	tac Tyr	ggg Gly	gtg Val	cct Pro 270	ttt Phe	gga Gly	816
ctt Leu	tta Leu	agc Ser 275	gac Asp	tgc Cys	cag Gln	gca Ala	tcc Ser 280	aag Lys	aca Thr	cca Pro	gaa Glu	ctg Leu 285	cac His	cgc Arg	tgg Trp	864
ctc Leu	agg Arg	atc Ile 290	aaa Lys	ctg Leu	tgg Trp	atc Ile 295	tcc Ser	acg Thr	gta Val	gcc Ala	ctt Leu 300	gcc Ala	ctg Leu	gtt Val	cct Pro	912
ttt Phe 305	ctg Leu	ctt Leu	ctc Leu	att Ile	ccc Pro 310	aag Lys	ttc Phe	gcc Ala	cgc Arg	tgg Trp 315	ttc Phe	tca Ser	gtg Val	cca Pro	tgg Trp 320	960
aag Lys	gtc Val	atc Ile	ttt Phe 325	gtc Val	ttt Phe	gct Ala	ctc Leu	ctc Leu	gcc Ala 330	ttt Phe	ctg Leu	ttt Phe	ttc Phe	act Thr 335	tcc Ser	1008
tgg Trp	tac Tyr	tct Ser	agt Ser 340	tat Tyr	gga Gly	ttt Phe	act Thr	cga Arg 345	cgt Arg	tgg Trp	aat Asn	tgc Cys	atc Ile 350	ctt Leu	atg Met	1056
agg Arg	aac Asn	cat His 355	gaa Glu	att Ile	atc Ile	cag Gln	cag Gln 360	cca Pro	atg Met	aaa Lys	gag Glu	gag Glu 365	aaa Lys	gta Val	gct Ala	1104
tcc Ser 370	ctc Leu	atg Met	ctg Leu	aag Lys	gag Glu	gca Ala 375	ctt Leu	gct Ala	ttc Phe	att Ile	gaa Glu 380	agg Arg	tac Tyr	aaa Lys	agg Arg	1152
gaa Glu 385	cct Pro	ttt Phe	ctc Leu	ctc Leu	ttt Phe 390	ttt Phe	tcc Ser	ttc Phe	ctg Leu	cac His 395	gta Val	cat His	act Thr	cca Pro	ctc Leu 400	1200
atc Ile	tcc Ser	aaa Lys	aag Lys	aag Lys 405	ttt Phe	gtt Val	ggg Gly	cgc Arg	agt Ser 410	aaa Lys	tat Tyr	ggc Gly	agg Arg	tat Tyr 415	ggg Gly	1248
gac Asp	aat Asn	gta Val	gaa Glu 420	gaa Glu	atg Met	gat Asp	tgg Trp	atg Met	gtg Val	ggg Gly	aaa Lys	atc Ile	ctg Leu 430	gat Asp	gcc Ala	1296
ctg Leu	gac Asp	cag Gln	gag Glu	cgc Arg	ctg Leu	gcc Ala	aac Asn 440	cac His	acc Thr	ttg Leu	gtg Val	tac Tyr 445	ttc Phe	acc Thr	tct Ser	1344
gac Asp	aac Asn	ggg Gly	ggc Gly	cac His	ctg Leu	gag Glu 455	ccc Pro	ctg Leu	gac Asp	ggg Gly	gct Ala 460	gtt Val	cag Gln	ctg Leu	ggg Gly	1392
ggc Gly 465	tgg Trp	aac Asn	ggg Gly	atc Ile	tac Tyr 470	aaa Lys	ggg Gly	ggc Gly	aaa Lys	gga Gly 475	atg Met	gga Gly	gga Gly	tgg Trp	gaa Glu 480	1440
gga Gly	ggg Gly	atc Ile	cgt Arg	gtg Val 485	cca Pro	ggg Gly	ata Ile	ttc Phe	cgg Arg 490	tgg Trp	ccg Pro	tca Ser	gtc Val	ttg Leu 495	gag Glu	1488
gct Ala	ggg Gly	aga Arg	gtg Val 500	atc Ile	aat Asn	gag Glu	ccc Pro	acc Thr	agc Ser	tta Leu	atg Met	gac Asp	atc Ile 510	tat Tyr	ccg Pro	1536
acg Thr	ctg Leu	tct Ser 515	tat Tyr	ata Ile	ggc Gly	gga Gly	ggg Gly 520	atc Ile	ttg Leu	tcc Ser	cag Gln	gac Asp 525	aga Arg	gtg Val	att Ile	1584
gac Asp	ggc Gly	cag Gln	aac Asn	cta Leu	atg Met	ccc Pro 535	ctg Leu	ctg Leu	gaa Glu	gga Gly	agg Arg 540	gcg Ala	tcc Ser	cac His	tcc Ser	1632
gac Asp 545	cac His	gag Glu	ttc Phe	ctc Leu	ttc Phe 550	cac His	tac Tyr	tgt Cys	ggg Gly	gtc Val 555	tat Tyr	ctg Leu	cac His	acg Thr	gtc Val 560	1680
agg Arg	tgg Trp	cat His	cag Gln	aag Lys	gac Asp	tgt Cys	gca Ala	act Thr	gtg Val	tgg Trp	aaa Lys	gct Ala	cat His	tat Tyr	gtg Val	1728

565										570										575										
act	cct	aaa	ttc	tac	cct	gaa	gga	aca	ggg	gcc	tgc	tat	ggg	agt	gga		1776													
Thr	Pro	Lys	Phe	Tyr	Pro	Glu	Gly	Thr	Gly	Ala	Cys	Tyr	Gly	Ser	Gly															
			580					585					590																	
ata	tgt	tca	tgt	tcg	ggg	gat	gta	acc	tac	cac	gac	cca	cca	ctc	ctc		1824													
Ile	Cys	Ser	Cys	Ser	Gly	Asp	Val	Thr	Tyr	His	Asp	Pro	Pro	Leu	Leu															
		595					600					605																		
ttt	gac	atc	tca	aga	gac	cct	tca	gaa	gcc	ctt	cca	ctg	aac	cct	gac		1872													
Phe	Asp	Ile	Ser	Arg	Asp	Pro	Ser	Glu	Ala	Leu	Pro	Leu	Asn	Pro	Asp															
	610					615					620																			
aat	gag	cca	tta	ttt	gac	tcc	gtg	atc	aaa	aag	atg	gag	gca	gcc	ata		1920													
Asn	Glu	Pro	Leu	Phe	Asp	Ser	Val	Ile	Lys	Lys	Met	Glu	Ala	Ala	Ile															
	625				630					635					640															
aga	gag	cat	cgt	agg	aca	cta	aca	cct	gtc	cca	cag	cag	ttc	tct	gtg		1968													
Arg	Glu	His	Arg	Arg	Thr	Leu	Thr	Pro	Val	Pro	Gln	Gln	Phe	Ser	Val															
				645					650					655																
ttc	aac	aca	att	tgg	aaa	cca	tgg	ctg	cag	cct	tgc	tgt	ggg	acc	ttc		2016													
Phe	Asn	Thr	Ile	Trp	Lys	Pro	Trp	Leu	Gln	Pro	Cys	Cys	Gly	Thr	Phe															
			660					665					670																	
ccc	ttc	tgt	ggg	tgt	gac	aag	gaa	gat	gac	atc	ctt	ccc	atg	gct	ccc		2064													
Pro	Phe	Cys	Gly	Cys	Asp	Lys	Glu	Asp	Asp	Ile	Leu	Pro	Met	Ala	Pro															
		675					680					685																		
tga																	2067													
<210> 95																														
<211> 688																														
<212> PRT																														
<213> Homo sapiens																														
<400> 95																														
Met	Leu	Ile	Ser	Gly	Arg	Glu	Glu	Asn	Gln	Ile	Asp	Ile	Ser	Lys	Thr															
1				5					10					15																
Thr	Glu	Val	Asp	Cys	Phe	Val	Val	Glu	Leu	Gly	Ser	Leu	His	Asn	Pro															
			20					25					30																	
Thr	Arg	Asn	Pro	Gln	Arg	Ile	Phe	Thr	Lys	His	Val	Ala	Thr	Lys	Ser															
		35					40					45																		
Ser	Ser	Ser	Lys	Cys	Gln	Leu	Asp	Gln	Gly	Gly	Lys	Ser	Leu	Val	Gln															
	50					55					60																			
Cys	Ile	Leu	Pro	Arg	Ser	Ser	Lys	Leu	Leu	Ser	Pro	Leu	Cys	Leu	Pro															
	65				70					75					80															
His	Pro	Cys	Gly	Ala	Leu	Leu	Leu	Tyr	Arg	Ser	Ser	Gly	Ile	Ala	Ser															
				85					90					95																
Ala	Leu	Ala	Ala	Phe	Thr	Asp	Ser	Leu	Ser	Arg	Ser	Cys	Trp	Leu	Ser															
			100					105					110																	
Val	Ser	Leu	Cys	Cys	Leu	Phe	Cys	Gly	Val	Asp	Gly	Thr	Phe	Met	Thr															
		115					120					125																		
Arg	Asn	Ala	Arg	Pro	Asn	Ile	Val	Leu	Leu	Met	Ala	Asp	Asp	Leu	Gly															
	130					135					140																			
Val	Gly	Asp	Leu	Cys	Cys	Tyr	Gly	Asn	Asn	Ser	Val	Ser	Thr	Pro	Asn															
	145				150					155					160															

Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala
165 170 175

Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg
180 185 190

Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala
195 200 205

Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr
210 215 220

Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly
225 230 235 240

Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr
245 250 255

His Pro Leu Asn His Gly Phe His Tyr Phe Tyr Gly Val Pro Phe Gly
260 265 270

Leu Leu Ser Asp Cys Gln Ala Ser Lys Thr Pro Glu Leu His Arg Trp
275 280 285

Leu Arg Ile Lys Leu Trp Ile Ser Thr Val Ala Leu Ala Leu Val Pro
290 295 300

Phe Leu Leu Leu Ile Pro Lys Phe Ala Arg Trp Phe Ser Val Pro Trp
305 310 315 320

Lys Val Ile Phe Val Phe Ala Leu Leu Ala Phe Leu Phe Phe Thr Ser
325 330 335

Trp Tyr Ser Ser Tyr Gly Phe Thr Arg Arg Trp Asn Cys Ile Leu Met
340 345 350

Arg Asn His Glu Ile Ile Gln Gln Pro Met Lys Glu Glu Lys Val Ala
355 360 365

Ser Leu Met Leu Lys Glu Ala Leu Ala Phe Ile Glu Arg Tyr Lys Arg
370 375 380

Glu Pro Phe Leu Leu Phe Phe Ser Phe Leu His Val His Thr Pro Leu
385 390 395 400

Ile Ser Lys Lys Lys Phe Val Gly Arg Ser Lys Tyr Gly Arg Tyr Gly
405 410 415

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Lys Ile Leu Asp Ala
420 425 430

Leu Asp Gln Glu Arg Leu Ala Asn His Thr Leu Val Tyr Phe Thr Ser
435 440 445

Asp Asn Gly Gly His Leu Glu Pro Leu Asp Gly Ala Val Gln Leu Gly
450 455 460

Gly	Trp	Asn	Gly	Ile	Tyr	Lys	Gly	Gly	Lys	Gly	Met	Gly	Gly	Trp	Glu
465					470					475					480
Gly	Gly	Ile	Arg	Val	Pro	Gly	Ile	Phe	Arg	Trp	Pro	Ser	Val	Leu	Glu
				485					490					495	
Ala	Gly	Arg	Val	Ile	Asn	Glu	Pro	Thr	Ser	Leu	Met	Asp	Ile	Tyr	Pro
			500					505					510		
Thr	Leu	Ser	Tyr	Ile	Gly	Gly	Gly	Ile	Leu	Ser	Gln	Asp	Arg	Val	Ile
		515					520					525			
Asp	Gly	Gln	Asn	Leu	Met	Pro	Leu	Leu	Glu	Gly	Arg	Ala	Ser	His	Ser
	530					535					540				
Asp	His	Glu	Phe	Leu	Phe	His	Tyr	Cys	Gly	Val	Tyr	Leu	His	Thr	Val
545					550					555					560
Arg	Trp	His	Gln	Lys	Asp	Cys	Ala	Thr	Val	Trp	Lys	Ala	His	Tyr	Val
				565					570					575	
Thr	Pro	Lys	Phe	Tyr	Pro	Glu	Gly	Thr	Gly	Ala	Cys	Tyr	Gly	Ser	Gly
			580					585					590		
Ile	Cys	Ser	Cys	Ser	Gly	Asp	Val	Thr	Tyr	His	Asp	Pro	Pro	Leu	Leu
		595					600					605			
Phe	Asp	Ile	Ser	Arg	Asp	Pro	Ser	Glu	Ala	Leu	Pro	Leu	Asn	Pro	Asp
	610					615					620				
Asn	Glu	Pro	Leu	Phe	Asp	Ser	Val	Ile	Lys	Lys	Met	Glu	Ala	Ala	Ile
625					630					635					640
Arg	Glu	His	Arg	Arg	Thr	Leu	Thr	Pro	Val	Pro	Gln	Gln	Phe	Ser	Val
				645					650					655	
Phe	Asn	Thr	Ile	Trp	Lys	Pro	Trp	Leu	Gln	Pro	Cys	Cys	Gly	Thr	Phe
			660					665					670		
Pro	Phe	Cys	Gly	Cys	Asp	Lys	Glu	Asp	Asp	Ile	Leu	Pro	Met	Ala	Pro
		675					680					685			